

## STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number:126106

TO: Ginny Portner

Location: REM/3B02/3C18

**Art Unit: 1645** 

Tuesday, July 06, 2004

Case Serial Number: 09/732091

From: Toby Port

**Location: Biotech-Chem Library** 

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

#### Search Notes

Dear Examiner Portner,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 



#### STIC-Biotech/ChemLib

196106

From:

Portner, Ginny

Sent:

Tuesday, June 29, 2004 6:07 PM

To:

STIC-Biotech/ChemLib

Subject:

RE: 09/732,091

try 09/732,091

Ginny Rortner Remsen Building Art Unit 1645 Room E03, B02 (571) 272-0862

-----Original Message-----

From:

STIC-Biotech/ChemLib

Sent:

Tuesday, June 29, 2004 4:23 PM

To:

Portner, Ginny

Subject:

RE: 09/732,081

There is no valid CRF for this Serial Number. Please provide us with another Serial Number from the Parent Application.

**LEONARD 22520** 

-----Original Message-----

Portner, Ginny From: Sent:

Tuesday, June 29, 2004 4:21 PM

To:

STIC-Biotech/ChemLib

**Subject:** 09/732,081 Importance:

Please search SEQ ID NO 3 and 4 with respect to polypeptides/proteins. The nucleic acid should be back translated to the polypeptide. Thanks.

Ginny Bortner Remsen Building Art Unit 1645 Room E03, B02 (571) 272-0862

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
ORLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

Query Match Best Local 9

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121

181 181 241 241

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disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. PQE/HP30 protein
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; Pred. No. 1.9e-118;
0; Mismatches 0;
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100.0%;
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96US-00630405.
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Matches 253; Conservative
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                                                                                                                                       1 MAXKYDRDLEFLKQLESSDLLDLFEVLVFGKDGERRHNEKLTSSIEYRRHGDDYAKYAER
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                                                             Length 253;
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Pred. No. 1.
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                                                         100.0%;
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Helicobacter sp. HP30 protein
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N-PSDB; AAD44535.
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                           Sequence 253 AA
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AAE26878;

RESULT 2

132

9 72

Gaps

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Length 265; Indels Cytoplasmic, vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope. Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter. Mellgaerd BL; or, Berglindh 1997-052306/05 WPI; 1997-052306/ N-PSDB; AAT67811 Smith D,

The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a

el Helicobacter proteins, HP30 and HP56, and nucleic acids encoding proteins, useful as vaccines for raising immune response in animals.

Tian J,

AAE26878

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AAC
AAE2
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BE Hell
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BE LOW
BE HELL

Novel

Disclosure; Page 122-123; 127pp; English.

us-09-732-091-4.rag

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The present sequence is a H. pylori cytoplasmic protein. The protein may identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 mucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest;
                                                                                                                                                                                                                                                                                                                                                                                           particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
Claim 61; Page 651; 1481pp; English
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GRGLSLAGNQVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 240
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Length 253;
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Score 1270; DB 2;
Pred. No. 1.4e-117;
1; Mismatches 1;
99.3%;
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Query Match
Best Local Similarity 99.2
Matches 251; Conservative
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AAW24673 standard; protein; 253 AA AAW24673 

AAW24673 RESULT

(first entry) 12-AUG-1997 H. pylori cytoplasmic protein, 4095342.aa.

Transmembrane, cytoplasmic; cell envelope, flagella, transport, secreted, periplasmic, chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle, vaccine, immunise; detection; antisense; inhibition.

Helicobacter pylori

WO9719098-A1

29-MAY-1997

96WO-US018542 15-NOV-1996; 95US-00561469 17-NOV-1995;

(ASTR ) ASTRA

Smith DH;

WPI; 1997-298052/27

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compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for acid sequences, and corresponding proteins, are also useful for modelecting the presence of Helicobacter species in a sample. Antisense in detecting the presence of Helicobacter species in a sample. Antisense mucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMFX vectors, while the overhang is not self-complementary. Therefore the linker sull not concatemerise nor will the cut vector re-ligate itself easily. The linker adapter inserts were ligated to each of the 20 pMFX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then sequenced. Note: The ORR protein reference number for this sequence was obtained from the related specification,
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                                                                                                                                                                              This sequence represents an H. pylori cytoplasmic protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate
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                                        Helicobacter pylori nucleic acid sequences and related proteins - used for diagnostics and therapeutics.
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Pred. No. 1.4e-117;
1; Mismatches 1; Indels (
                                                                                                                              Claim 18; Page 184; 235pp; English.
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Best Local Similarity 99.2
Matches 251; Conservative
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181 GRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 240 Æ AAW20866 standard; protein; 256 241 ANGDKKSLQIESI 253 ANEDKKSLQIESV 241 RESULT 5 셤 à g

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AAW20866

AAW20866;

18-JUL-1997 (first entry)

H. pylori cytoplasmic protein, 12ge20305orf30.

Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis 

Helicobacter pylori.

WO9640893-A1

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Best Local Similarity:
Query Match:
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The present sequence is a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by methanically shearing the bacterial DNA. The sequences were analysed for by computer evaluation. To identify likely H. pylori antigens for vaccine by computer, the amino acid sequences predicted room various ORF were analysed for significant homology to other known or exported membrane analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts

4400

Indel8:

Length:
Matches:
Conservative:
Mismatches:

6.94e-134 1270.00 99.60% 99.21% 94.14%

Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.

Claim 61; Page 651; 1481pp; English.

Mellgaerd BL;

OI,

D, Berglindh

Smith

(ASTR ) ASTRA AB.

WPI; 1997-052306/05. N-PSDB; AAT67811.

95US-00487032.

07-JUN-1995; 01-APR-1996;

TIGGATITGITIGAGGIGCITGITITIGGIAAAGACGCGAAAAAAGACACAAIGAAAA 120 CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA 180 240 360 300 100 420 20 140 9 9 80 1 ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA 61 IleAlaGluGluLeuGlnTyrTyrGlySerAenSerPheAlaSerPheIleLysGlyGlu GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC 301 AAGAAAACTGAAACGACTTTAATTGAACAAACATGCTTTCTAAAATCTTAGAAAGT TTGGAAGAAATGGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAC US-09-732-091-3 (1-759) x AAW20486 (1-253) 19 361 121 41 181 241 à 셤 g ð ò g a à à g

480

421 ACGGACAATTTAAACAGACAACCTTAAGGCGCGCGACTTTAACGTGTTTTAAAATGGGG

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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori

XAX CX X X X X X C X H

WO9640893-A1 19-DEC-1996 06-JUN-1996;

H. pylori cytoplasmic protein, 4095342.aa.

(first entry)

29-JUL-1997

AAW20486;

Z

AAW20486 standard; protein; 253

RESULT 3 RESULT

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5, 2004, 03:11:28 ; Search time 34 Seconds (without alignments) 2316.318 Million cell updates/sec
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1. /cgn2_6/ptodata/2/jubpaa/PCT_NEW_PUB.pep:*

2. cgn2_6/ptodata/2/jubpaa/PCT_NEW_PUB.pep:*

3. /cgn2_6/ptodata/2/jubpaa/NS06_NEW_PUB.pep:*

4. /cgn2_6/ptodata/2/jubpaa/US06_PUBCOMB.pep:*

5. /cgn2_6/ptodata/2/jubpaa/US06_PUBCOMB.pep:*

6. /cgn2_6/ptodata/2/jubpaa/NS08_PUBCOMB.pep:*

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9. /cgn2_6/ptodata/2/jubpaa/US08_PUBCOMB.pep:*

10. /cgn2_6/ptodata/2/jubpaa/US08_PUBCOMB.pep:*

11. /cgn2_6/ptodata/2/jubpaa/US09_PUBCOMB.pep:*

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13. /cgn2_6/ptodata/2/jubpaa/US09_NEW_PUB.pep:*

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16. /cgn2_6/ptodata/2/jubpaa/US108_PUBCOMB.pep:*

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16. /cgn2_6/ptodata/2/jubpaa/US106_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1276540 seqs, 311283816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                           Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli Sequence 44, Appli Sequence 9162, App Sequence 9163, App Sequence 7699, App Sequence 7699, App Sequence 144, Appl Sequence 120, Appl Sequence 17, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl	Sequence 43832, A Sequence 191043,
SUMMARIES	US-09-732-091-4 US-09-732-091-4 US-10-335-977-9162 US-10-335-977-9163 US-10-335-977-9164 US-10-335-977-7699 US-09-335-977-7699 US-09-882-227-414 US-09-732-091-19 US-09-732-091-19 US-09-732-091-19 US-09-732-091-19 US-09-732-091-19	US-10-282-122A-43832 US-10-437-963-191043
DB		12
f Query Match Length DB	   1   1   1   1   1   1   1   1   1 	1009 815
ł Query Match	1000.0 1000.0 99.3 99.3 99.3 96.0 100.7 110.5 111.1	7.7
Score	11270 11270 11270 1270 7220 7252 1252 1988 1550	98.5
Result No.	14 2 2 4 4 2 6 1 4 2 2 1 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14 15

Sequence 76490, A.		740	Sequence 14395, A	Sequence 54543, A	Sequence 29, Appl	Sequence 169, App	Sequence 220, App		Sequence 52737, A	Sequence 47217, A	Sequence 5229, Ap	251, 7	Sequence 12141, A	Sequence 197045,	682,	1075	22205	Sequence 107, App				590	7664,	Sequence 749, App	50,	š	Ç.	Sequence 199420,	4
US-10-282-122A-76490	US-10-369-493-42	US-10-032-585-7400	US-10-156-761-14395	US-10-282-122A-54543	US-09-919-172-29	US-10-205-219-169	US-10-341-434-220	US-10-341-434-230	US-10-282-122A-52737	US-10-282-122A-47217	US-10-369-493-5229	US-09-815-242-5251	US-09-815-242-12141	US-10-437-963-197045	US-10-412-699B-682	US-10-369-493-1075			US-10-425-114-43207	US-10-437-963-122954		US-1	US-10-032-585-7664	US-10-289-762-749	US-10-253-904-50	US-10-282-122A-58561	US-10-260-708-60	US-10-424-599-199420	US-09-817-764-4
12	15	14	14	12	σ	14	15	15	12	12	15	φ	0	16	12	15	12	15	12	16	12	15	14	15	74	7.5	12	12	σ
916	373	701	1102	517	2125	2649	2649	2649	1196	610	430	966	1009	889	241	1847	629	1163	573	744	820	820	1089	281	260	869	384	482	552
7.6	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.3	7.3	7.2	7.2	7.2	7.2	7.2	7.2	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9
97	96.5	96.5	96.5	95	95	95	95	95	93.5	693	92.5	92.5	92.5	92	91.5	91.5	90.5	90.5	90	06	90	90	90	89.5	89.5	89.5	89	88.5	88.5
16	17	138	13	O O	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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61 IAEELQYYGSNSPASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LEEMJDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                      APPLICANT: Tian, Jing-Hui
APPLICANT: Tian, Jing-Hui
APPLICANT: Tian, Jing-Hui
APPLICANT: Jackson, W. James
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT FILING DATE: 2000-12-07
NUMBER OF SRQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1279; DB 9; Length 253; Best Local Similarity 100.0%; Pred. No. 4.8e-115; Matches 253; Conservative 0; Mismatches 0; Indels 0.
                  Sequence 4, Application US/09732091
Patent No. US20020107368A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Helicobacter sp.
                                                                                                                                                                                                                                                                                                                                                                             253
US-09-732-091-4
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Publication No. US20040052799A1
GENERAL INFORMATION: WITH et al
APPLICANT: DOUGLAS SMITH et al
IITLE OF INVENTION: RUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                        APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-197
ATTORNEY, AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REPERBUCE/DOCKET NUMBER: 37,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)27-7400
TELEPRAX: (617)742-4214
INFORMATION FOR SEC ID NO: 9162:
SEQUENCE CHARACTERISTICS:
                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...253
; SEQUENCE DESCRIPTION: SEQ ID NO: 9162:
US-10-335-977-9162
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 253 amino acids
TYPE: amino acid
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STATE: Massachusetts
COUNTRY: USA
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Matches 251; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LEEMDDEEVKEMCDELSIKNTDNIARQALSAATLTIFKMGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEMDDEEVKEMCDELSIKNTDNINRQALSAATLTLFKWGGFKSYQLAVIVANAVAKTIL 192
GRGLSLAGNOVLTRILSFLIGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRIKTQQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                      APPLICANT: Tian, Jing-Bui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
FILE REPERBING: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
UNWERN FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1279; DB 9;
Pred. No. 5.1e-115;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIF: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9162, Application US/10335977 Publication No. US20040052799A1 GENERAL INFORMATION:
                                                                                                                                                           RESULT 2
US-09-732-091-44
Sequence 44, Application US/09732091
Parent No. US20020107368A1
GENERAL INFORMATION:
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ANGDKKSLQIESI 253
                                                 253
                                                                                              241 ANGDKKSLQIESI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-44
                                                   ANGDKKSLQIESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-335-977-9162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 44
LENGIH: 265
       181
                                                   241
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61 IABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEMDDEEVKEMCDELSIKNTDNINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLILFKMGGFKSYQLAVIVANAVAKTIL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MAYKYDRDLEPLKOLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%; Score 1270; DB 12; 99.2%; Pred. No. 3.6e-114; tive 1; Mismatches 1;
                                                                                                                                                                                            APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAMB/XEY: misc feature
LOCATION: (B) LÖCATION 1...256
SEQUENCE DESCRIPTION: SEQ ID NO: 9164:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT
                         ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 256 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 9164: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 10031
                                                                                                                                              SOFTWARE: UNIX CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 ANEDKKSLQIESV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ANGDKKSLOIESI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.2
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-335-977-9164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTIFKMGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRGLSLAGNQVLTRILSFLIGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IAEELQYYGSNSFASFIKGEGVLYKBILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 120
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION:
BELATING TO HELLCOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1270; DB 12;
Pred. No. 3.6e-114;
          MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34/993,002
FILING DATE: 17-DEC-197
ATTORNEY/AGENT INFORMATION:
NAME: MANGER: 36,207
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.3%; Score 1270; I
Best Local Similarity 99.2%; Pred. No. 3.6e
Matches 251; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...253
SEQUENCE DESCRIPTION: SEQ ID NO: 9163:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 253 amino acids
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ANGDKKSLQIESI 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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US-10-335-977-9164
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of Polynucleotides US20030158396Alel Helicobacter Polypeptides in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 GSNSFASFIKGEGVLYKBILCDVCDKLKVNYNKKTETTLIEGNMLSKILERSLEEMDDEE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 VKEMCDELSIKNTDNL---NRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTILGRGL- 184

    LEFLKRISSSDLXDLFDALVYDEDGTLRMNBELTSLTEYQRYGKDYAKYPRRIAEELQRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEELQYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 SLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLK 237
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                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY-AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
RECERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)72-27400
TELEFAX: (617)72-27400
TELEFAX: (617)72-27414
INFORMATION FOR SEC ID NO: 7698:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...237
SEQUENCE DESCRIPTION: SEQ ID NO: 7698:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Omb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynu
TITLE OF INVENTION: Brocding No. US20030158
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/647002
CURRENT APPLICATION NUMBER: US/09/882,227
PRIOR APPLICATION NUMBER: US 08/902,615
                                                                                            COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Helicobacter pylori
                     ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 414, Application US/09882227; Publication No. US20030158396A1; GENERAL INFORMATION:
                                                                                                                                                                                                                     FILING DATE: 30-Dec-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 237 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal APPLICANT: Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-335-977-7698
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US-09-882-227-414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 EVKEMCDELSIKKTDNL---NRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTILGRGL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 YGSNSFASFIKGEGVLYKEILCOVCDKLKVNYNKKTETTLIEQNMLSKILERSLEEMDDE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 -SLAGNQVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRIK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 SSVVGKVALKKTLDILAGPIGWVITGALVSÍNLÁGPAÝRVTVPÁCVLVATLRKK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.3%; Pred. No. 2.8e-61;
Matches 141; Conservative 36; Mismatches 53; Indels
                                                                  ZIP: 02109-1875
COMPUTER READABLE FORM:
COMPUTER: IEM PC Compatible
COMPATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
RAPELCATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...248
; SEQUENCE DESCRIPTION: SEQ ID NO: 7699:
US-10-335-977-7699
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GTN-018
TELEPONAUNICATION INFORMATION:
TELEPHONE: (617) 727-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 7699:
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7698, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-335-977-7698
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Gaps

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Length 38;

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Sequence 19, Application US/09732091
Fatent No. US200201073681
GENERAL INFORMATION
APPLICANT: Time of Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TITLE OF INVENTION: Hereof
FILE REFERENCE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT PILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 NRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTILGRGLS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NRQALSAATLTLFKWGGFKSYQLAVIVANAVAKTILGRGLS 41
                                                                                                                                                                                                      1 DYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCD 38
                                                                                                                                                                              53 DYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCD 90
                                                                                           Query Match 15.5%; Score 198; DB 9; I
Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 15.2%; Score 194; DB 9; 1
I Similarity 100.0%; Pred. No. 2.1e-11;
41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LEEMDDEEVKEMCDELSIKATDNIARQALS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Ver. 2.1
                              ORGANISM: Helicobacter sp. US-09-732-091-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT

ORGANISM: Helicobacter sp.

US-09-732-091-18
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   US-09-732-091-19
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US-09-732-091-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 19
LENGTH: 41
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SEQ ID NO 18
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             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                      62 NYNEESATSLIBQNMLSKLLKDSLERMSRREIKELCNELGMTKIDKVIGENKQVLIASTL 121
                                                                                                                                                                                                                                                                                38 NEKLTSSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGCVLYKEILCDVCDKLKV 97
                                                                                                                                                                                                                                                                                                   2 NEDL'INSTEYKRYGHDYARXPRIAEELQHYGGNSFANFFRDEGLYKEILCDACDHLKV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/09732091

Sequence 20, Application US/09732091

GENERAL INFORMATION:
APPLICANT: Tian, Ving-Hui
APPLICANT: Tian, Ving-Hui
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TITLE OF INVENTION: Helicobacter proteins, gene sequences
TITLE OF INVENTION: Helicobacter proteins, gene sequences
CURRENT APPLICATION NUMBER: US/09/732,091

CURRENT FILING DATE: 2000-12-07

NUMBER: Patentin Ver: 2.1

SSOFTWARE: Patentin Ver: 2.1
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APPLICANT: Walker, Richard I.
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
IITLE OF INVENTION: thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                             36.9%; Score 472.5; DB 10; Length 155; 63.3%; Pred. No. 1.8e-37; Live 22; Mismatches 29; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 VGWIITGVWTAIDIASPAYRVTIPACIVVATLRLKTQQANGDKKSLQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 TLFKAGGSHSYALAVSVADAMWRQTLG 148
PRIOR FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 7969-088
CURRENT PELLING NUMBER: US/09/732,091
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09732091
Patent No. US20020107368A1
GENERAL INFORMATION:
                                                                                    LENGTH: 155
TYPE: PRT
CRGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 105.0
Marches 49; Conservative
                                                                                                                                                                                                                                      93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r TYPE: PRT
PORGANISM: Helicobacter sp.
US-09-732-091-20
                                                                                                                                                                                                            Best_Local Similarity
Matches 93; Conserv
                                                                                                                                                    US-09-832-227-414
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US-09-732-091-20
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US-09-732-091-17
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Gaps

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Length 41;

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Sequence 18, Application US/09732091
Patent No. US20020107368A1
GENERAL INFORMATION:
APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TITLE OF INVENTION: thereof
FILE REFERENCE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 11.9%; Score 152; DB 9; Soir Similarity 100.0%; Pred. No. 1.6e-07; 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LEEMDDEEVKEMCDELSIKNTDNLNRQALS 150
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16;

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated Wit
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: 18/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 191043
                                                                                                                                                                                                                                                                                                                                       708 YNNIDLELNEQSIEMEMSRLNLTDDNDINEILAWRGEQEE-----LEOKR--DTYKK 756
                                                                                                                                                                                                                                                                                                                                                                                               57 YAERIABELQYYGSNSFASFIKGEGVLYKBILCDVCDKLKVNYNKKTE--TTLIE---- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               805 HYQCQNNINKTQSIVSHINYLAQBLKDQQBIFQLABIVSGKNNKNLTLENFVLIYYLDQI 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSAATLTLFKWGGFKSYQLAVIVANAVAKTILGRGLS-----LAGNQVLTRTLSFLT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               865 IAQANIRLATMSD-NRYQL-----IRREAVSHGLSGLEIDVFDLHSNK--SRHISSLS 914
                                                                                                                                                                                                                                                                                                                                                                                                                                              757 RYHEFEMÉLA-----RLESLTKD-----KELLDS--DKLKDEVEQKKEKMNTLIDEYSAV 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 ---AEBLQYYGSNSPASFIKGEGVLYKBII.CDVCDKLKVNYNKKTETTLIBONMLSKILE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIRYKRHGDDYAKYAERI 61
                                                                                                                                                                                                                                                                                        5 YDRDLBP-----LKQLESSDLLDLFEVLVFGXDGEKRHNEKLTSSIEYKRHGDDYAK
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQANGDKKSLQIESI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLN-----
                                                                                                                                                                            7.7%; Score 98.5; DB 12; Length 1009; 22.5%; Pred. No. 3.2; ive 45; Mismatches 83; Indels 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INPORMATION: Clone ID: PAT_MRT4530_8739C.1.pep
US-10-437-963-191043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 191043, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                        TYPE: PRT

CRGANISM: Staphylococcus aureus
US-10-282-122A-43832
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                 Query Match
Best Local Similarity 22.5%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-10-437-963-191043
             SEQ ID NO 43832
LENGTH: 1009
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PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A.
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                       APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
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                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
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                                               Sequence 16, Application US/09732091
Patent No. US20020107368A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Helicobacter sp. US-09-732-091-16
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                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 16
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Search completed: July 5, 2004, 03:13:58 Job time : 34 secs

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Skelton, J.; Stevens, Salmonella enterica se
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                                   'S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2011
A; Athors: Parry, C.; Quai, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Ste A; Title: Complete genome sequence of a multiple drug resistant Salmonella enter A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Accession: AC0503
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-237 < PAR>
A; Residues: 1-237 < PAR>
C; Genetics: C; Genetics: GB:AL513382; PIDN:CAD01163.1; PID:g16501293; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-237 <HAY>
A;Residues: 1-237 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33434.1; PID:g13359467; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.7%; Score 265; DB 2; Length 23 32.6%; Pred. No. 1.4e-12; ive 40; Mismatches 101; Indels
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: | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : : | 1 : 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Best Local Similarity 32.6
Matches 79; Conservative
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Best Local Similarity 30.8
Matches 76; Conservative
                              S.; O'Gaora,
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Cipacian Caratta Protein Novil - Escherichia coli (Strain K-12)
Cipacian Caratta Protein Novil - Escherichia coli (Strain K-12)
Cipacian Caratta Caratta Discussion 17-Sep-1997 #text_change 01-Mar-2002
Cipacian Caratta Discussion Discussion Discussion Discussion Caratta Caratta Discussion Discuss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ιρ
                                                                                                                                                                                                                 NYNKKTETTLIEGNMISKILERSLEEMDDEEVKEMCDELSIKNTDNL---NRQALSAATL 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                        TLFKAGGSBSYALAVSVADAMVROTLG 148
                                                                                                                                                                                                                                                                                                                                                           TLFKMGGFKSYQLAVIVANAVAKTILG 181
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Cippedies: Yersinia pestis
Cipate 102-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
Cipate 102-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
Cipate 102-Nov-2001 #sequence_revision N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. R. Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Bavies, R.M.; Dougan, G. A., M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, R.M.; Drogan, G. Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
Airitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Object: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Cispecies: Testing 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1009 <KUR>
A;Cross-references: GB:BA000018; PID:g13701144; PIDN:BAB42439.1; GSPDB;GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   757 RYHEFEMEIA-----RLESLIKD-----KERLLDS--DKLKOBYEQKKEKMINTLIDEYSAV 804
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A;Residues: 1-282 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92208.1; PID:g15980920; GSFDB:GN00175
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                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SA1181 [imported] - Staphylococcus aureus
         Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83; Indele
                                                                                                                                                                                                                                I MAYRYDSDLEFLKRLSSSDLKDLFDALVYDEDGTLRMNE 39
    Score 133; DB 2; L. Pred. No. 0.00096; 5; Mismatches 8;
                                                                                                                                                                                       1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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10.4%;
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                                                                                                Conservative
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                                                       Similarity
26; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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    Query Match
Best Local &
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C,Species: Helicobacter pylori
C,Species: Helicobacter pylori
C,Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C,Accession: E4718
R;Tomb, J.F.; White, C.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Wallin, E.; Hayes, W.S.; Borodovsky, M.; Fujii, C.; Bowman, C.; Watthey, L. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64718
A;Accession: F64718
A;Actession: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: 055481
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MJD:21074935; PMID:11206551
A;Accession: C85481
A;Accession: C85481
A;Accession: C85481
A;Residues: Draiminary
A;Rolecule type: DNA
A;Residues: 1-237 <20>
A;Cross-references: GB:AS005174; NID:g12512689; PIDN:AAG54311.1; GSPDB:GN00145; UMGP:200
C;Generics:
A;Cross-references: SE:AS005174; NID:g12512689; PIDN:AAG54311.1; ASPDB:GN00145; UMGP:200
A;Reperimental source: strain 0157:H7; substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (strain O157:H7, substrain
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                                                           VIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPAC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LÍÁGELŐHFGGDSIÁNKLRGHGKLÝRAÍLEDVSKRÍKLKADKEMSTFEÍBGGLÍEGFÍRN 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Gaps
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    Escherichia coli

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Best Local Similarity 30.84
Matches 76; Conservative
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A,Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A,Reference number: A81250; MUID:20150912; PMID:10688204
A,Accession: CB1380
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-311 cPAR>
A,Crossreferences: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74209.1; PID:g69676enetics:
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Job time : 14 secs
             2000
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           Nature 403, 665-668,
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A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conserved hypothetical protein XYPU_2790 [imported] - Mycoplasma pulmonis (strain UAB CT c)Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: G90546
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A95512; MUD:21267165; PMID:11353084
A;Accession: G90546
A;Accession: G90546
A;Accession: G90546
A;Accession: G90546
A;Residues: 1-1099 «XUR»
A;Residues: 1-1099 «XUR»
A;Residues: 1-1099 «XUR»
A;Conserreferences: GB:AL445566; PID:g14089692; PIDN:CAC13452.1; GSPDB:GN00153
A;Experimental source: strain UAB CIIP
C;Genetics
A;Genetic code: SGC3
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                                                                                                                                                                                                                                                               FIKMS--LIKDQFISEVTRYSSDITAKVNTGEITTETAIKLLDKELSDIRNQDESMTRER 110
                                                                                                                                                                                                                                                                                                                   129 VKE-MCDELSIKNTDNLNRQALSAATLILFKMG-GFKSYQLAVI----VANAVAKTILGR 182
                                                                                                                                                                                                                                                                                                                                                111 VKQAVIIKAŠVKENNNVERNEV----INLVFAGVGFVTAGLQIVAGVGWVGSVVGSIPGT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||:
54 FHNDLKIFEGSLKNIAGKDGQNLYEIVIDKEQMKKHKNEIVEKETNEVYNEFFIDPKTKK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 YNKKT-----ETTLIEQNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALS 150
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                                                                                                                                                                                               ----NSIASK 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 A----ATLTLF-KMGGFKSYQLAVIVANAVAKTILGRGLSLAGNOVLTRTLSFLTGPV 203
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                                                                                                                                              19 DILDLFEVLVFGKDGEK-RHNEKLTSSIBYKRHGD-DYAKYAERIAEELQYYGSNSFAS-
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                                                                    Length 282;
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                                                                  DB 2;
4.9;
                                                                                                                                                                                                                                                                                                                                                                                                         183 GLSLAG-NQVLTRILSFL---~TGPVGWIITGV-
                                                                ; Score 98; DB ; Pred. No. 4.9; 34; Mismatches
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                                                              7.7%;
ilarity 24.7%;
Conservative 34
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Best Local Similarity 22.2
Matches 53; Conservative
                                                         Query Match
Best Local Similarity
                                                                                                      58;
C,Genetics:
A,Gene: YP02963
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probable ATP /GTP binding protein Cj0411 [imported] - Campylobacter jejuni (strain NC: C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Out. 2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: A81386
R;Parkhill, J: Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar: Mature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals ]
A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74247.1; PID:g696: A;Bxperimental source: serotype O2, strain NCTC 11168
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                              40 KLTSSIEYKRH-----GDDYAKYAERIAEELQYY---GSNSFASFIKGEGVLYKEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - KRHGDDYAKY
                                                                                                                   53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 EFLKQLESSDLL---DLFEVLVFGKDGEKRH----NEKLTSSIEY---
                                                                                                                37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         |: :: | :: | |: | || || :| | || || 254 GLDVLBIEPPMKNHPLLSIKNKENLIITPHVAWASKEALNA 294
                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                   Query Match 7.6%; Score 97.5; D
Best Local Similarity 23.0%; Pred. No. 6;
Matches 37; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 97.5; D 25.4%; Pred. No. 18; tive 27; Mismatches
C;Superfamily: phosphoglycerate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                      120 SLEEMDDBEVKEMCDELSIKNTDNL--
                                                                                                                                                                                                                                                                              89 CDVCDKLKVN--YNKKTETTL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 LSKILERSLEEMDDEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.4%
Matches 43; Conservative
```

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

July Run on:

5, 2004, 03:08:23; Search time 12 Seconds (without alignments) 1097.812 Million cell updates/sec

Title: Perfect score:

US-09-732-091-4 1279 1 MAYKYDRDLEFLKQLESSDL......LRLKTQQANGDKKSLQIESI 253 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	026107 helicobacte	09z124 helicobacte	in						acuifex ae	Q01457 lactococcus		003001 homo sapien	qallu	O60136 bacillus me	P31956 arthrobacte	P46064 caenorhabdi	P77994 thermotoga				Q07068 ciona intes				P45274 haemophilus		P46633 cricetulus	033662 streptococc	۲-	PilS01 qallus qall		P07901 mus muschlu	sus 5
SUMMARIES	ΠD	HELP	YF88 HELPJ	YF87 HEL.PY	YF87 HELPJ	YAAW ECOLI	YAAW ECO57	HS9A_BRARE	SECA_TREPA	BIOF AQUAE	ABIC LACLA	YC09 CAMJE	BPA1 HUMAN	REST CHICK	PAC BACME	PAC ARTVI	RCQ1 CAEEL	RPSD THEMA	GATB_METJA	HS9A_HORSE	YJK9 YEAST	TPM1_CIOIN	LA BOVIN	Y705_CHLPN	GATE_SULSO	AMPN HAEIN	NESG HUMAN	HS9A CRIGR		SSM4 SCHPO	HS9A CHICK	HS9A HUMAN	HS9A MOUSE	HS9A_PIG
	DB	٦	r-d	roi	Н	Н		Н	Н	Н	Н	Н	-	Н	Н	Н	Н	ч	Н	Н	Н	Н	Н	Н	Н	Н	П	Н	Н	H	Н	Н	-	ч
	Length	253	253	209	209	237	237	726	916	373	344	517	3214	1433	802	805	892	399	472	719	1769	284	404	280	633	869	386	732	371	670	728	731	732	732
*	Ouery Match		99.3	-	49.3	20.7			7.6	,		•	7.4				•		7.2	•	•		•	7.0	•				6.9				6.8	
	Score	1279	1270	637	630	265	262	105	97	96.5	g5, 5	92	92	94.5	93,5	92.5	92.5	91.5	91.5	91.5	91.5	16		0 0 0 0	י רכ	89.5		88.5	88		<u> </u>	87.5	~	r~
,	No.	1	73	m	4	2	G	7	œ	σv	10	er e	12	13	14	15	91	17	B :	61	50	H 5	7.7	23	4.1	525	56	27	58	29	30	31	32	m) m)

O8rgh4 fusobacteri	09zke4 helicobacte	O9zl53 helicoharte	028994 archaenglob	O9kxr6 streptomyce	025149 helicobacte	027944 archaeoglob	P38853 saccharomyo	O51578 borrelia bu	O8k914 buchnera an	096935 plasmodium	09nv70 homo sapien
HIPG FUSNN	PRIA HELPJ	HMCT HELPJ	CARB ARCFU	CARB_STRCO	PRIA HELPY	YN40 ARCFU	KEL1 YEAST	EX5B_BORBU	HFLK_BUCAP	AMP1_PLAFO	SEC3_HUMAN
н	Н	Н	₩	Н	Н	Н	-	Н	٦	Н	Н
607	619	686	1076	1102	619	633	1164	1169	411	1085	894
6.8	6.8	6.8	6.8	6.8	6.7	۲., ن	6.7	6.3	6.3	6.3	9.9
R T	86.5	86.5	86.5	86.5	98	98	98	98	85.5	85.5	82
34	35	36	37	38	39	40	41	42	43	4.4	<u>2</u> . τυ

## ALIGNMENTS

1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFCKDGEKRHNEKLTSSIEYKRHGDDYAKYAER 60 Gaps o O Length 253; Indels Query Match 100.0%; Score 1279; DB 1; Best Local Similarity 100.0%; Pred. No. 9.1e-88; Matches 253; Conservative 0; Mismatches 0; à

g &

61 IAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 120

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                                                    GRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 NYNESSATSLIEQNWLSKLIKDSLEKMSRREIKELCNELGMTNIDKVIGENKQVLIASTL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 NYNKKTETTLIEQNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNL---NRQALSAATL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIR=26695 / ATCC 700392;
STRAIR=26695 / ATCC 700392;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.,
Loftus B., Richardson D., Dodson K., Khalak H.G., Glodek A.,
McKenney K., FirzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.B., Googayne J.D., Utterhack T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Mallin B.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 NEDLINSTEYKRYGHDYAKYPRRIABELQHYGGNSFANFFRDEGVLYKEILCDACDHLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 NEKLISSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria; Epsilonproteobacteria, Campylobacterales;
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the UPF0174 family. CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; UPF0174; 1.
1. protein; Complete proteome.
209 AA: 23069 XM; F98D3FB8F3F62323 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.8%; Score 637; DB 1; 60.3%; Pred. No. 2.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
49.8%; Score 637; DB
Best Local Similarity 60.3%; Pred. No. 2.3e
Matches 123; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000656; AAD08626.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005367; UPF0174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein HP1587.
                                                                                                                                               241 ANGDKKSLOIESI 253
                                                                                                                                                                                                          241 ANEDKKSLOIESV 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori.";
Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bairoch A.;
Unpublished observations
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03667; UPF0174;
Hypothetical protein; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; HP1587;
                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                       YF87 HELPY
             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              026106;
                                                                                                                                                                                                                                                                                                                                               YF87_HELPY
                                                                            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            180
                                                                                                                                                                       180
                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                GRGLSLAGNQVLTRILSFLTGPVGWIITGVWTAIDIAGPAXRVTIPACIVVATLRLKTQQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LEEMDDEEVKEMCDELSIKNTDNIARQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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LEEMDDEEVKBMCDELSIKNTDNINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                LEEMDDEEVKEMCDELSIKNTDNINRQALSAATLTLEKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                      GRGLSLAGNOVLTRILSFLIGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 IAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAYKYDRDLEFLKQLESSDLJDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127158B2B1A2036A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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99.2%; Pred. No. 4.2e-87;
ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the UPF0174 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein JHP1494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interproj procession of the process 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastric pathogen Helicobacter pylori.";
Mature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99120557, PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence comparison of
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TLFKMGGFKSYQLAVIVANAVAKTILGR-GLSLAGNQVLTRTLSFLTGFVGWIITGVWTA 213
                  TLFKAGGSHSYALAVSVADAMVRQTLGHXACYVVGKVALKKTLGVLAGPIGWVITGALVS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYNKKTETTLIEGNWLSKILERSLEEMDDEEVKEMCDELSIKNTDNL---NRQALSAATL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLFKMGGFKSYQLAVIVANAVAKTILGRGL-SLAGNQVLTRTLSFLTGPVGWITTGVWTA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLFKAGSSHSYALAVAVADAMVRQTLGHGLSSVVGKVALKKTLJILAGPIGWVITGALVS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NEELTSLTEYORYGHDYAKYPRRIAEELORYGGNSFANFFRDEGVLYKEILCDACDHLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 NEKLTSSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKV
                                                                                                                                                                                                                              Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                  Alm R.A., Ling L. S.L., Moir D.T., King B.L., Brown B.D., Doig P.C. Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                     two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 209;
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209 AA; 22907 MW; CGEC950CDD424CAF CRC64;
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59.8%; Pred. No. 7.7e-40;
iive 32; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence comparison of two unrelated igastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- SIMILARITY: Belongs to the UPF0174 family.
                                                                                                                                                                (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                          209 AA.
                                                   IDIAGPAYRVTIPACIVVATLRLK 237
                                                                IDIAGPAYRVTIPACIVVATLRLK 237
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001571; AAD07072.1; -. PIR; A71800; A71800.
                                                                                                                                                                                                      Hypothetical protein JHP1493.
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Pfam; PF03667; UPF0174; 1.
Hypothetical protein; Complete
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Best Local Similarity
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16-OCT-2001
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ekropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 YLNDSDLDFLQHCSEEQLANFARLLTHNEKGKTRLSSVLMRNELFKSMEGHPEQHRRNWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=KIZ. / MG1655, MEDLINE=97426617; PubMed=9278503; MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Bscherichia,
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                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE=94003405; PubMed=8400364;
James R., Dean D.O., Debbage J.;
James R., Gean D.O., Debbage J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: Belongs to the UPF0174 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X67700; CAA47934.1; -.
PIR; CA6421; C64721.
ECGGene; EG14340; vaw.
InterPro; IPR005367; UPP0174.
Pfam; PP03667; UPP0174; 1.
Hypothetical protein; Complete protecome.
CONFLICT 190 190 L. -> F (IN REF. 1).
SEQUENCE 237 AA; 26665 MW; A36682BZEA116747 CRC64;
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125 TWKKMDEBHKQEFLHAVDARVNELEELLPLLMKDKLLAKGVS---
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                   P756IT; Q47290;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yaaW.
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STANDARD;
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                                                                                                                                                                                                                Escherichia coli.
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RESULT

RESULT 5 YAAW\_ECOLI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 VIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDLAGPAYRVTIPAC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YKYDRULEFIKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKR---HGDDYAKYAE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli O157.H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLNDSDLDFLQHCSEEQLANFARLTHNEKGKTRLSSVLARNELFKSYRGHPEQHRRNWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=0157.H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Merca N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett T., Klink S., Boutin A., Shao X., Miller L.,
Grocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Weich R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005367; UPF0174.

Pfam; PF03667; UPF0174; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 237 AA; 26681 MW; A25482B2EA116759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 20.5%; Score 262; DB 1; L
Local Similarity 30.8%; Pred. No. 1.5e-12;
nes 76; Conservative 45; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the UPF0174 family.
                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FAPPOTECTION protein yaam
FAPPOTECTION CROS012.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; Pubmed=11258796;
                                                                                                                                                                                                                                                                                                                                     Enterobacterlaceae; Escherichia
NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE005178; AAG54311.1; -. EMBL; AP002550; BAB33434.1; -.
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; C85481; C85481.
PIR; C90630; C90630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                            YAAW ECO57
P58316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
YAAW ECOS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                HID DESCRIPTION OF STREET AND SERVICE COLOR OF STREET AND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GVLYK-BILCDVCDKLKVNYNK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 DYVSRMKDTQKHIYYITGETKDQVANSAFVERLRKAGLBVIYMIBPIDBYCVQQLKEYDG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 KTETTLIEQNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGG 161
                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinoperygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the zebrafish and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEELQYYGSNS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the heat shock protein 90 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%; Score 105; DB 1; Length 726; 21.4%; Pred. No. 2.5; ive 41; Mismatches 75; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 36-136 FROM N.A.
MEDLINE=95071389; PubMed=7980538;
Krone P.H., Sass J.B.;
"HSP 90 alpha and HSP 90 beta genes are present in the zebz are differentially regulated in developing embryos.";
Biochem. Biophys. Res. Commun. 204:746-752(1994).
-!- FUNCTION: Wolecular chaperone. Has ATPase activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMEL, 155586; AAA97518.1; ...
PTR, JC2343; JC2343.
TRSP, PO7900; 1BYO.
TRESP, PO7900; 1BYO.
TREPPO; IPRO03594; ATPbind_ATPase.
InterPro; IPRO03594; ATPbind_ATPase.
TherPro; IPRO0404; HSP90.
TherPro; IPRO1818; HATPase c; 1.
Than; PPO2518; HATPase c; 1.
TherPro; PRO0775; HEATSHOCK90.
SMART; SM00387; HATPase c; 1.
TRESPITE; PS00298; HSP90; 1.
TRESPITE; PS00298; HSP90; 1.
TRESPITE; PS00298; HSP90; 1.
TRESPITE; PS00298; HSP90; 1.
TherPromer T26 AA; B3361 MM; F7DEBBEFIFBC9CEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lele Z., Hadfi S., Sass J.B., Krone P.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                           75-UT-1999 (Rel. 38, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-Spock protein HSP 90-alpha.
HSP90A OR HSP90.
726 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF068773; AAC21567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Conservative
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                                                                   ---IMKDILDKKIEKVTVSNRLVSSPCCIVTSTYGWTANMERIMKSQALR 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Involved in protein export. Interacts with the secY/secE subunits. SecA has a central role in coupling the hydrolysis of ATP to the transfer of pre-secretory periplasmic and outer membrane proteins across the membrane (By similarity). SUBUNIT: Part of the prokaryotic procein translocation apparatus which comprise secA, secB, secB, secE, secG, and secY (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                              162 FKSYQLAVIVANAVAKTILGRGLS--LAGNQVLTRTLSFLTGPVGWIIT-----
                                                                                                                                                                                                                                                                                                                                                                                        Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01312; SECA; 1.
Protein transport; ATP-binding; Membrane; Translocation; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SUBCELLULAR LOCATION: Cytoplasmic side of plasma membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                      ----GVWTA---IDIAGPAYRVTIPACIVVATLRLKTQQANGDK 245
----NIVS-VTKEGLELPEDEREKKKØDELKAK-YENLCK-
                                                                                                                                   615 DNSTMGYMTAKKHLEIN-----PAHPIVETLREKAEAEKNJK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     916 AA; 103779 MW; EA5561F6EE7C65AE CRC64;
                                                                                                                                                                                                                                                                                             Last sequence update}
                                                                                                                                                                                                                                         916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SIMILARITY: Belongs to the secA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Last sequence 28-FEB-2003 (Rel. 41, Last annotatio Preprotein translocase secA subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004027; SEC C motif.
InterPro; IPR000185; SecA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02810; SEC-C; 1.
Pfam; PF01043; SecA_protein; 1.
PRINTS; PR00906; SECA.
TIGREAMS; TIGR00963; secA; 1.
                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001217; AAC65365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 281:375-388(1998).
                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; E71330; E71330.
                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Spirod
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                   SECA OR TP0379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spirochete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; TP0379;
¥
                                                                                                                                                                                                                                     TREPA
                                                                                                        209
                                                                     568
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                                                                                                                                                                                                                                     SECA TRE
083394;
                                                                                                                                                                                                                    SECA
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                                                                                                                                       B.
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Length 916;

Score 97; DB 1; Pred. No. 13;

7.6%;

Best Local Similarity

Query Match

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13;
                                                                                                                                             415
                                                                                                                                                                                   147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on the European Bioinformatics Institute. There are no restrictions on the Use by non-profit institutions as long as its content is in no ways modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBoib.ch).
                                                                                                          104
                                                                      367
                                                                                                                                                                                                  48
                                                                                                                                                                                                                                                      189
                                                                                                                             EH-----IRIAQRNRTWATITFQNFFR-----WYKGLSGWTGTADTEALELNKIYKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: 6-carboxyhexanoyl-CoA + L-alanine = 8-amino-7-coronamoate + CoA + CO(2).
-!- COFACTOR: Pyridoxal phosphate (By similarity).
-!- PATHWAY: Biotin biosynthesis; first step.
-!- SIMILARITY: Belongs to class-II of pyridoxal-phosphate-dependent aminotransferases.
                                       --- KRHNEKLTSSIEYK
                                                                     311 FKY---IHYFTQALRAHLLYRADVDYVVKDGQVQIVDEFTGRILEGRRYSDGLHQALEAK
                                                                                                        RHGDDYAKYAERIAESLQYYGSNSFASFIKGEGVLYKBI--LCDVCDKLKVNYNK--KTE
                                                                                                                                                                                 -LSIKNTENLNRQ
                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
8-amino-7-oxononancate synthase (EC 2.3.1.47) (AONS) (8-amino-7-ketopelargonate synthase (C 2.3.1.47) (AONS) (Reamino-7-AONT)
7-KAP synthetase) (1-keto-8-amino-pelargonic acid synthetase)
7-KAP synthetase) (1-alanine--pimelyl CoA ligase).
Aquifex aeOlicus.
       Gaps
                                                                                                                                                                                                                                                      ---VAKTILGRG--LSLAGN
                                                                                                                                                                                                                                                                                      -----ALLRTRGVKHEVLNAKNHAREALITAEAGAKGSVTIATNMAGRGTDIKLGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98196666; PubMed=9537320; Deckert G., Warren P.V., Gasaterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRIDOXAL PHOSPHATE (BY SIMILARITY).
     16;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02400; ALA synthase; 1.
Pfam; PF00155; aminotran 1 2; 1.
TIGREPAM; TIGROBS8; bioF; 1.
PROSITE; PS00599; AA TRANSFER CLASS 2; 1.
Biotin biosynthesis; Transferase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42532 MW; 536B34A5D5F84401 CRC64;
 67;
                                                                                                                                                                                                                                                  148 ALSAATLTLFKMGGFKSYQL-----AVIVANA
                                                                                                                                                                                                                                                                                                                                                                               7
   Mismatches
                                                                                                                                                                             105 TTLIEQNM-LSKILERSLEEMDDEEV-KEMCDE-
                                   3 YKYDRDLEFLKQLESSDLLDLFEVLVFGKDGE-
                                                                                                                                                                                                                                                                                                                                                                               373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; G70355; G70355.
HSSP: P12998; 1BS0.
InterPro; IPR003408; Ala synthase.
InterPro; IPR0040839; Aminotrans I/II.
InterPro; IPR001917; Aminotrans I/II.
                                                                                                                                                                                                                                                                                                                                                                              PRT;
   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000699; AAC06836.1; -.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004723; BloF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
52;
                                                                                                                                                                                                                                                                                                                                                                            BIOF AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=VF5;
                                                                                                      49
                                                                                                                                          368
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SEQUENCE
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F_AQUAE
 Matches
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     --- OKVELVISRO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AYKYDRDIBFLKQLESSDILDIFEVLVPGKDGEKRHNEKLTS-SIEYKRHGDDYAKYAER 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 TETTLIEQNMISKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLEKMGGE
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN.NCTC 11168;
MEDINEZCTC 11168;
MEDINEZCTC 11168;
MEDINEZCO150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
White genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Nature 403:665-668 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                 Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
                                                   7.4%; Score 95; DB 1; Length 517;
145 FINDYNIDIGNGLDFRFNLFESNQWFSITYNSSKYKGKN-LTKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6A799602ED363A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the UPF0144 family. -!- SIMILARITY: Contains 1 HD domain. -!- SIMILARITY: Contains 1 KH domain.
                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0144 protein Cj1209.
                                                                                                                                                                                                          517 A.A.
                                                                                           163 KSYQLAVIVANAV-AKTILGRGLSLAGNOV 191
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                                                                                                               246 -SEELVVILINSLYVRRGLGLGIELIGTNL
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InterPro; IPR006675; Unchar_HDIG.
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Hypothetical protein; Transme:
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HAMAP, MF_00335; -; 1.

InterPro; IPR006674; HD.

InterPro; IPR04087; KH_dom.
                                                                                                                                                                                                          STANDARD;
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SMART; SM00322; XH; 1.
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Pfam; PF00013; KH; 1.
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517 AA;
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                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=197;
                                                                                                                                                                                                        CAMJE
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Q9PNB6;
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YC09 CAMJE
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                                                                                                                                                                                                                          119 ASIIDGVRLSKAQKRVPKHKDYBBLBEPLK----KNRKKFRRVLI--ITDTVFSMDGDVA 172
                                                                                                                                  BRIABEL-QYYGSNSFASFIKG-------EGVLYKEILCDVCDXLKVNYNKKTE 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 RDLEFLKQLESSD-----LLDLFEVLVFGKDGEKRHNEKLTSSIEYKR-----HGDD 53
                                                                                          173 DLKRLTOICEEYDCMLYIDEAHTTGTIGKGGLDYFGIEHKEYIIVMGTLSKALGSYGAFV
                                                                                                                                                                                                TILIEQNALSKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLILFKAGG---
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
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                                                                                                                                                              RELEBKLASFKGTESCVLFGSGFLANGTIPALVEEGDL---VLSD----ELNH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Durmaz E., Higgins D.L., Klaenhammer T.R., "Molecular characterization of a second abortive phage resistance gene present in Lactococcus lactis subsp. lactis ME2.";
                                        77;
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             Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.5%; Score 95.5; DB 1; Length 344;
        ; Score 96.5; DB 1; Length 37; Pred. No. 4.7; 40; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
                                                                                                                                                                                                                                                                                                                                                         233 CGTKLLID-----YLVNKARSLIPST-SLPPSVCAGAKKAIEI 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 AA; 40128 MW; AA6E41E71B4A003C CRC64;
                                                                      9 LEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHG-
                                                                                                                                                                                                                                                                                                                             TGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQANGDKKSLQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1993 (Rel. 27, Last sequence update) Abortive phage resistance protein abiC. ABIC OR PRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA
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        7.5%;
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                                        Conservative
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                         Similarity
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Les 50; Conserv
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                                      64;
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ID ABIC_LACLA
      Query Match
Best Local S:
Matches 64
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us-09-732-091-4.rsp

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Stanley J.R.;
  161
                     -- DWCDKLKVNYNKKTBTTL-- 107
                                                                                                                            201 BFAARLINVINIKNDELKGRIIGKEGRNV--KTLE-------MVLGVDIIID-----
                                                                                                   --IEQNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGG
                                                                                                                                                                            FKSYQLAVIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJURE=33346896; PubMed=8345227;
Elgart G.W., Stanley J.R.;
"Cloning of the 5' mRNA for the 230-kD bullous pemphigoid antigen by
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Bullous pemphigoid antigen 1 isoforms 1/2/3/4/5/8 (230 kDa bullous pemphigoid antigen) (Hemidesmosomal plaque protein) (Dystonia Eusculorum protein) (Fragment).
BPAGI OR DMS OR DT OR KLAA0728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Keratinocytes;
MEDLINE=92011493; PubMed=1717441;
Sawamura D., Li K., Chu M.-L., Uitto J.;
"Human bullous pemphigoid antigen (BPAG1). Amino acid sequences deduced from cloned cDNAs predict biologically important peptide segments and protein domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                         Q03001; Q12825; Q13266; Q13267; Q13775; Q96J76; Q96QT5; Q9UGD7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-645 FROM N.A. (ISOFORMS 1 AND 2).
TISSUB-Fetal brain, and Retina;
MEDLINE=96121394; Pubmed=857575;
Brown A., Dalpe G., Mathieu M., Kothary R.;
"Cloning and characterization of the neural isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka T., Parry D.A.D., Klaus-Kovtun V., Steinert P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Pineal gland;
Geerts D., Sonnenberg A.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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                     IAEELQYYGSNSFASFIKGEGVLYKEILC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rapid amplification of cDNA ends.";
J. Invest. Dermatol. 101:244-246(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 266:17784-17790(1991)
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WEDLINE=91286285; PubMed=1712022;
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                                                                                                                                                                                                                                                                                        --DTPGAIIVSCFNL 257
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                                                           LOOBBEKLKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human)
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"Comparison of molecularly cloned bullous pemphigoid antigen to desmoplakin I confirms that they define a new family of cell adhesion junction plaque proteins.";
J. Biol. Chem. 26:12555-12559(1991).
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                                                                                                                                                                                                                                                                                                                                                                                          Diaz L.A., Franke W.W.;
"The hemidesmosomal plague. I. Characterization of a major
constituent protein as a differentiation marker for certain forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2462-3214 FROM N.A. (ISOFORM 8).
MEDLINE=94280413; PubMed=8010969;
Hopkinson S.B., Jones J.C.;
Hopkinson of a second protein product of the gene encoding human epidermal autoantigen.";
Biochem. J. 300:851-857(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang H.-Y., Chaffotte A.-F., Thacher S.M.;
"Structural analysis of the predicted coiled-coil rod domain of cytoplasmic bullous pemphigoid antigen (BPAGI). Empirical localization of the N-terminal globular domain-rod boundary.";
J. Biol. Chem. 271:9716-9722(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragments;
                                                                                                                                                                                                                                                                                                                                                 S., Magin T.M., Krieg T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=4;
IsoId=203001-4; Sequence=VSP_005054, VSP_005056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q03001-2; Sequence=VSP_005053, VSP_005055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q03001-6; Sequence=VSP_005062, VSP_005063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSP 005065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCUNIT: Homodimer.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=10;
Comment=18oforms 1, 2, 5 and 8 are or may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2287-3214 FROM N.A. (ISOFORM 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=3; Synonyms=1e;
IsoId=Q03001-3; Sequence=VSP_005054,
VSP_005061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence=VSP 005064,
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                                                                                                                                                                                                                                      SEQUENCE OF 2160-2767 FROM N.A. MEDLINE=91216368; PubMed=2090522; Owaribe K., Kartenbeck J., Stumpp Diaz L.A., Franke W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB=Keratinocytes;
MEDLINE=89067122; PubMed=2461961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epithelia."; Differentiation 45:207-220(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96199235; PubMed=8621649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=7; Synonyms=EB;
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IsoId=Q03001-5;
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Gaps

38;

62; Indels

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2075 SFRDEKELEKLOICÓRKSDHLKEQFEKSHEQLLQNIKABKENNDKIQRLNBELEKSNECA 2134
                                                                                                                                                                                                                                                                                             98 -NYNKKTETTLIEQNMLSKI--LERSLEEMDD--EBVKEMCDELSI-----KNTDNLNR 146
                                                                                                                                                                 2 AYKYDRDLEFLK--QLESSDLLDLF----EVLVFGKDGEKRHNEKLTSSIEYKRHGDDYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pectoralis muscle;

MEDLINE=99002898; PubMed=9784600;

Griparic L., Keller T.C. III;

"Identification and expression of two novel CLIP-170/Restin isoforms expressed predominantly in muscle.";

Biochim. Biophys. Acta 1405:35-46(1998).

-!- FUNCTION: SEEMS TO BE A INTERMEDIATE PILAMENT ASSOCIATED PROTEIN THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES (BY SIMILARITY).

-|- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE CYTOSKELED WITH THE COMMENT OF THE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98137792; PubMed=9469933;
Griparic L., Volosky J.M., Keller T.C. III;
"Cloning and expression of chicken CLIP-170 and restin isoforms.";
Gene 206:195-208(1998)
                                                                           DB 1; Length 3214;
                                                                                                                                                                                                                                                            56 KYAERIAEEL--QYYGSNSFASFIKGEG---VLYKEILCDVCDKLKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=042184-2; Sequence=VSP 000761;

Name=3; Synonyms=CLIP-170(11);

IsoId=042184-3; Sequence=VSP 000762, VSP_000763;

Name=4; Synonyms=CLIP-170(11+35);

IsoId=042184-4; Sequence=VSP 000764;

-!- SIMILARITY: Contains 2 CAP-Gly domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               042164, 042228, 057563, 057564, 15-UL-1998 [Rel. 36, Created) 15-UL-1998 [Rel. 36, Last sequence update) 10-OCT-2003 [Rel. 42, Last annotation update) Restin (Cytoplasmic linker protein-170) (CLIP-170).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 17-1139 FROM N.A. (ISOFORMS 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bvent=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                          IsoId=C42184-1; Sequence=Displayed;
                                             Query Match
Best Local Similarity 25.4x
Best-Local 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- ALTERNATIVE PRODUCTS:
                           1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                         1091
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                      DOMAIN
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REST_CHICK
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GO; GO:0005737; C:cytoplasm; IBP.

GO; GO:0005737; C:cytoplasm; IBP.

GO; GO:00057010; F:structural constituent of cytoskeleton; IBP.

GO; GO:00057010; F:structural constituent of cytoskeleton in IBP.

GO; GO:00057010; F:structural constituent of cytoskeleton organiza.

DR GO; GO:00057010; P:cytoskeleton organization and biogenesis; TAS.

IN therPro; IPR00110; P:cytoskeleton organiza. .; IBP.

IN therPro; IPR0010; P:cytoskeleton orga
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                          PROSITE; PS00019; ACTININ 1; 1.
PROSITE; PS00020; ACTININ 2; FALSE_NEG.
PROSITE; PS50021; CH; 2.
Antigen; Actin-binding; Coiled coil; Repeat; SH3 domain; Structural protein; Cycoskeleton; Cell adhesion; Calcium-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENTRAL FIBROUS ROD DOMAIN
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ACTIN-BINDING
                                                                      IsoId=094833-1; Sequence=External;
                              IsoId=094833-3; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CH 1.
CH 2.
SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
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AY032900; AAK63130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M69225; -; NOT ANNOTATED CDS.
EMBL; L11690; AAA52288.1; -.
EMBL; U31850; AAC50243.1; -.
EMBL; U31831; AAC50244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AY032900; AAK63130.1;
EMBL, AY032901; AAK63131.1;
EMBL, M63618; AAA35606.1;
EMBL; KS8677; CAA41528.1;
EMBL; U04850; AAA3538.1;
EMBL; U04850; AAA35184.1;
EMBL; U04850; AAA57184.1;
EMBL; U04850; AAA57185.1;
PIR, IS6317; A40937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY032901; AAK63131.1; -.
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                                                  Name=10
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYN-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12114980;
Yang S., Huang Y.H., Huang X.D., Li S.Y., Yuan Z.Y.;
"High expression of penicillin G acylase gene from Bacillus megaterium
in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KYDRDLEFLKQLESSDLLDLFEV--LVFGKDG-----EKRHNEKLTSSIEYKRHGDDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 237542; CAA85774.1; -
EMBL; AF161313; AAD45609.1; -
PIF; 549252; S49252.

MEROPS; 5455.001; -
InterPro; IPR002692; Peptidase 545.

Ffam; PF01804; Penicil amidase; I.

Hydrodase; Antibiotic resistance; Zymogen; Calcium-binding; Signal.

SIGNAL
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                                                                                                                                                                                                                                                                                anion +
                                                 STRAINSATCC 14945,
MEDLINE=95180705; PubMed=7875576,
Martin L.M., Prieto A.M., Cortes E., Garcia J.L.;
Martin L.M., Prieto A.M., Cottes E., Garcia J.L.;
"Cloning and sequencing of the pac gene encoding the penicillin acylase of Bacillus megaterium ATCC 14945.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENICLILIN G ACYLASE ZYMOGEN.
PENICLILIN G ACYLASE ALPHA SUBUNIT.
SPACER PEPTIDE.
PENICLILIN G ACYLASE BETA SUBUNIT.
BY SIMILARITY.
CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
                                                                                                                                                                                                                                                       Acta Biochim. Biophys. Sin. 31:601-603(1999).
-!- CATALYTIC ACTIVITY: Penicillin + H(2)O = a fatty acid anion aminopenicillanat.
-!- COFACTOR: Binds 1 calcium ion per subunit (Potential).
-!- SUBCMIT: Heterodimer of an alpha chain and a beta chain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.3%; Score 93.5; DB 1; Length 802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA -> YKS (IN STRAIN CA4098)
877CA0564E50DFBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.3%; Score 93.5; DB 1; Length 80
Best Local Similarity 21.8%; Pred. No. 20;
Matches 62; Conservative 39; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T -> W (IN STRAIN CA4098).

T -> K (IN STRAIN CA4098).

T -> K (IN STRAIN CA4098).

T -> S (IN STRAIN CA4098).

A -> T (IN STRAIN CA4098).

P -> Y (IN STRAIN CA4098).

C -> P (IN STRAIN CA4098).

D -> P (IN STRAIN CA4098).

I -> A (IN STRAIN CA4098).

T -> K (IN STRAIN CA4098).

T -> K (IN STRAIN CA4098).
                                                                                                                                                                                                                                                                                                                                similarity).
-!- SUBCELLULAR LOCATION: Extracellular (Potential).
-!- SIMILARITY: Belongs to peptidase family S45.
           Misainmurhag Hoiji 32:215-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
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802 AA;
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      [See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1072 AEBULQ-----TMEKUTKEKDAIHQEKIETLASLENSRQINBKLONELDMLKQNNLKNEE 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1127 ELTKSKELLINLENKKVEELKKEF-----EALKLAAAQ------KSQQLAALQEE 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IABELQYYGSNSFASFIKGEGVLYK---BILCDVCDKLKVNYNKKTETTLIBONMLSKIL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E----RSLEEMDDEEVKEMCDELSIKNTDNLARQALSAATLTLFKMGGFKSYQLAVI-VA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                       Coiled coil; Repeat; Alternative splicing. CAP-GLY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAC BACME STANDARD; PRT; BUZ AM.
Q60136; Q9S463;
16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last sequence update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
(Penicillin G amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                  S -> GGSSKVS (in isoform 3).
/FIId=VSP 000763.
T -> RRRQISEDPENT (in isoform 4).
K -> R (IN REF. 2; AAC03547).
E -> V (IN REF. 2; AAC03548).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%; Score 94.5; DB 1; Length 1433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECURNCE FROM N.A. STRAIN-ATCC 14945; KANG J.H., Kim S.J., Park Y.C., Hwang Y., Yoo O.J., Kim Y.C., "Nucleotide sequence of the penicillin G acylase gene from Bacillus megaterium and characteristics of the enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1433 AA; 161026 MW; 5631CE8683498E23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                          RQISEDPEN (in isoform 3)
/FTId=VSP_000762.
                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                               Wissing (in isoform 2). /FIId=VSP 000761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.4%; Pred. No. 34; ive 36; Mismatches
entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                   CAP-GLY 2.
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                                                                                                                                                                                                                                                                                                          Missing
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                                        Cytoskeleton; Microtubule;
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1353
1427
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Bacteria; Firmicutes
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VARSPLIC
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CX NCBI
CX NCBI
RR SEQUE
RC STRAI
RA RANG
RT BACIL
RT BA

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us-09-732-091-4.rsp

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89 SKDEQSRRDGYSNKEIKKOMIDGLDRQPKELIAKFAEGISRYVNEALKDPDDKLSKEFHEY 148
                                                    --KILERSLEEMDDEEVKEMCDELSIKN- 140
                                                                                                                   -----SYQLAVIVANAVAK 177
                                                                                                                                            209 PSAPTSIVSEGKPKRDSSSQSLQILSSAVIKASEKVGKERENFVQTSEELGLPIKIGSNA 268
                                                                                149 QFLPQKWTSTDVVRVYMVSMTYFMDNHQELXNAEILAKLEHEYGTEVSRXXFDDLVWKND
                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
(Penicillin G amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; 545.001;
InterPro; IPR002692; Peptidase_S45.
Pfam; PF01804; Penicil amidase; 1.
Hydrolase; Antibiotic resistance; 2ymogen; Calcium-binding; Signal.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLIRE=94259306; PubMed=8200542;
Konstantinovic M., Marjanovic N., Ljubijankic G., Glisin V.;
Konstantinovic M., Marjanovic N., Ljubijankic G., Glisin V.;
Konstantinovic M., Marjanovic N., Ljubijankic G., Glisin V.;
Gene 143:79-83(1994).";
-!- CATALYTIC ACTIVITY: Penicillin + H(2)O = a fatty acid anion + aminopenicillanate.
-!- COPACTOR: Binds I calcium ion per subunit (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENICILLIN G ACYLASE ZYMOGEN.
PENICILLIN G ACYLASE ALPHA SUBUNIT.
SPACER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENICILLIN G ACYLASE BETA SUBUNIT.
BY SIMILARITY.
CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
                                                                                                                                                                                  178 TILGRGLSLAGNQVLTRTLSFLTGP-VGWIITGVWTAIDIAGPAY 221
                                                                                                                                                                                                         269 AIVGSEKSATGNALL----FSGPQVGFVAPGFLYEVGLHAPGF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9863E58C526C85D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
SUBCELLULAR LOCATION: Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to peptidase family S45.
                                                                                                                                                                                                                                                                                                        802 AA.
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92113 MW;
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PIR; I39665; I39665.
HSSP; P06875; LAJQ.
                                                                                                                                                                                                                                                                                                      STANDARD;
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265
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177
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802 AA;
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Best Local Similarity
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Gaps

177;

7.2%; Score 92.5; DB 1; Length 802; larity 21.8%; Pred. No. 24; Conservative 39; Mismatches 107; Indels 77

62;

Best Loca Matches

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89 SYDEQSRRDGYSNYRIXKWIDGLDRQPRELIAKFAEGISRYVNEALKDPDDKLSKEFHEY 148
                                                                                                                   ----KKTETTLIEQNMLS------140
                                                                                                                                      KYAERIABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYN-- 100
                                                                                                                                                                              ---TDNLNRQALSAATLTLFXMGGFK-----SYQLAVIVANAVAK 277
                                                                                                                                                                                               209 PSAPTSIVSEGKPKRESSSQSLQKLSSAVIKASEKVGKERENFVQSSEELGLPLKIGSNA 268
                                88
      55
                    4 KYDRDLBFLKQLESSDLLDLFEV--LVFGKDG-----BKRHNEKLTSSIBYKRHGDDYA
                                                                                                                                                                                                                                    178 TILGRGLSLAGNQVLTRTLSFLTGP-VGWIITGVWTAIDIAGPAY 221
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5, 2004, 03:06:48; Search time 29 Seconds (without alignments) 2752.624 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                              US-09-732-091-4
                                                                                                                           July
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1017041 seqs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1017041 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SPIREMBL 25:\* •• Database

sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* unclassified: \* vertebrate:\* sp\_organelle:\*
sp\_phage:\*
sp\_plant:\* sp\_rvirus:\* sp\_bacteriap:\* sp\_archea:\* sp\_bacteria:\* sp\_archeap:\* sp rodent:\* fungi:\* E G 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ORYGNA CALL	OBSETA Shinella FI	OSFICT PROPERTY	025108 heliochacte	ORiant placeodium	Obroad thousand	Ogdiba omoshoson	OSMET STREET	College alaceted g	payson prasmoutam	Olyhmo heliophacta	OSBOJO DEGLECOMACCE	OBital paeduculas	Carjar prasmoutum	Despired Property	COPPER MUSICAL TO	Vissus astyanax ra
SUMMARIES	, QI	OBXGV3	083534	QBFLC7	026108	OBIANI	OBR9Z4	OBDIH4	OBMX30	OBIKGB	P87397	O7VHM0	08821.0	281722	043633	09DB34	07ZZ19	, i
		16	16	16	16	Ŋ	16	16	'n	'n	13	16	16	2	4	- [	13	
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من	Query Match	20.7	20.3	20.3	10.4	8.2	8.1	8.0	8.0	7.9	7.9	7.8	7.8	7.7	7.7	7.7	7.7	
	Score	265	260	259	133	105	103.5	102.5	102	101	100.5	99.5	99.5	66	66	66	9	
	Result No.	1	7	m	4	Ŋ	Q	7	α	თ	10	11	12	13	14	15	16	

SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=CT18;

Nature 413:852-856(2001).

Q99ud0 staphylococ	Q8zc19 yersinia pe	Q8sdw1 bacteriopha	Q98qt2 mycoplasma	OBi297 plasmodium	OBihv4 plasmodium	Ogbic9 campvlohart	Ogni 94 campo Chart			Osiecs plasmodium	O63768 Caenorhabdí	O97mm5 rlostriding	ORilz2 rlasmodium	OSTICO methanosard	OBrh57 fuscharteri	Ogzigg borrelia bu	OB41b2 malue domes	OSi589 plasmodium	097uf7 sn1folobus		09khu3 helicobacte		Of 167 caenorhandi	OBBEN2 organism		OBPA17 streettocost		
oane60	Q8ZCL9	OBSDW1	Q98QT2	Q81297	8.IHY4	Q9PIC9	09PI94	O9ARO9	082707	BIEQS	51768	097MM5	OBILZ2	OBTPC2	OBRH57	09Z188	084LB2	281589	Q97UF7	051577	29 KHU3	27YSES	791190	08S6N2	09PPG7	OBEGJ7	08E143	Q96XT6
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7.7	7.7	7.7	7.7	7.7	7.7	9.7	5.6	7.6	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7,3	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.2	-, 5	7.2	7.2
98.5	86	86	90	90	eņ en	97.5	97.5	97.5	96.5	96.5	96	96	Q.	95.5	94.5	94	94	93.5	93	93	93	92.5	92.5	92.5	95	92	92	95
17	æ ;	Ť.	20	21	22	23	24	25	26	23	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	<b>4.</b>

## ALIGNMENTS

SPECIES S. typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; WEDLINE=21534946; PubMed=11677609; MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Haterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JMR-2003 (TrEMBLrel. 24, Last annotation update)
Hypochetical protein (Positive regulator for sigma H (Sigma 32)
promoters, permitting growth at high temperature). 237 AA PRT; J. Bacteriol. 185:2330-2337(2003). [2] Bnterobacteriaceae; Salmonella,
NCBI\_TaxID=601, 602; PRELIMINARY; Salmonella typhi, and Salmonella typhimurium. SEQUENCE PROM N.A. Q8XGV3 RESULT 1 **08XGV3**  Ŋ

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169 VIVANAVAKTILGRGISLAGNOVLTRILSFLTGPVGWILTGVWTAIDIAGPAYRVTIPAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 SLEEMDDE------EVKEMCDELSIKNTDNINRQALSAATLTIFKMGGFKSYQIA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YXYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKR---HGDDYAKYAE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIAEBLQYYGSNSFASFIKGEGVLYKBILCDVCDKLKVNYNKKTETTLIBQNMLSKILER
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Wasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner P.R.;
"Extensive mosaic structure revealed by the complete genome sequence
      WEDLINE=22590274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhwa G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perra N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Complete genome sequence and comparative genomics of Shigella flexneri serctype 2a atrain 24577"; Irfect. Immun. 71:2775-2786(2003).

EMBL; AG015039; AAN1678.1; BENEL, AG015039; AAN1678.1; BENEL, AG015039; AAN1678.1; InterPro; IPR005367; UPP0174; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 TWKKWDEEHKQEFLHAVDARVNELEELLPLLMKDKLLAKGVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 AA; 26709 MW; 95509A1BCB8B4CF5 CRC64;
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5727 MW; B8C190712375B31D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein yaaw.
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

EMBL; AR016755; AAN76816.1;

InterPro; IPR005367; UPF0174.

Hypothetical protein; Complete proteome.

SEQUENCE 237 AA; 26727 WW; B8C190712375831D CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.3%; Score 260; DB 16; 30.8%; Pred. No. 6.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Pred. ....rive 44; Mismatches
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ses 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 IVVATLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 LQIACLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAAW OR COOLE.
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OBFLC7;
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CQ8FLC7
DQ CRFL
AC CQ8FL
DT 01-M
DT 01-J
DE HYPO
CD BESCH
COC ENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 KILERSLEEMDDEEVKEMCDELSIKATDNIARQALSAATLTIFK-MGGFKSYQLAVIVAN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 HFLRHTWQRWDAAHKQBFLQAVDAKVSELEELLPLLMKDRSLAKGVSHLLSTQLTRILRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 AVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVWAT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 HAAMSILGHGL-IRG------AGLGGPVGAALMGVKA---MSGSAYRVTIPAVLQIAC 227
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                           Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Bakera S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jageis K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica servoar IPAD.
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang Y., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Shigella flexmeri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.7%; Score 265; DB 16; Length 237; Best Local Similarity 32.6%; Pred. No. 2.6e-12; Matches 79; Conservative 40; Mismatches 101; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE016834, AA067744.1, -.
EMBL; AE028693; AAL18974.1; -.
EMBL; AL627265, CA001163.1; -.
InterPro5 IFR065367; UPP0174.
Fram; PF03667; UPP0174; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 237 AA; 26515 MW; 184ADE026EA5BCA9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AA.
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
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MEDLINE=21534947; PubMed=11677608;
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01-JUN-2003 (TrEMBLE). 24,
01-OCT-2003 (TrEMBLE). 25,
Putative oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                Nature 413:848-852(2001)
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Shigella flexmeri
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Q835R4; Q835R4

RESULT 2

9 Gaps 36; 20.3%; Score 259; DB 16; Length 237; 30.9%; Pred. No. 7.5e-12; Live 44; Mismatches 91; Indels 36 Query Match Best Local Similarity 30,84, 28;

Indels

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542 EKKEBEKIMKKI.-YSEHPDLVKDIMNYEKEYAEKRNILINNIKKRKTIKTIN-RYKN---- 595
                                                                                                                                                                                                                                                                                                                                                                                                                       34 EKRHNEKLTSSIEYKRHGD---DYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCD
                                                                                                                                  Pain A., Hall N.,
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                              Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacter tengcongensis.
Parreria: Firmicutes; Clostridia; Thermoanaerobacteriales;
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MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

A Chen Y., Xue Y., Lai X., Huang L., Dong W., Ya Chen Y., Xue Y., Lai X., Huang L., Dong X., Ma Y., A Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Genome Res. 12:689-700(12002).

MEMBL; AB013102; AAM24658.1;

GO; GO:0009124; C:flagellar hook (sensu Bacteria); IEA.

GO; GO:000374; E:motor activity; IEA.

MINEPPO; IRR01055; Flag hook.
                                                                                                                                                                                                                     1245 AA; 147911 MW; D856486AFDFE4DDF CRC64;
                                                                                                                          Seeger K., Murphy L., Harris D., Berriman M., Pain A., F
Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL8445/7; CAD51332.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L protein; Complete proteome.
403 AA; 46116 MW; 60C22B9FBBS1A56F CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein TTE1436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
                                                                                                                                                                                                                                                            DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                  91 VCDKLKVNYNKKTETTLIEQNMLSKILERSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Clostridia, Thermoanae.
Thermoanaerobacteriaceae, Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 AA
                                                                                                                                                                                                                                                                                          21; Mismatches
                                                                                                                                                                                                                                                        Score 105; D:
Pred. No. 32;
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20.1%; Pred. No. 9.8;
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                                                                                                                                                                                                                                                        8.2%;
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DEISSKDHDNMN 665
                                                                                                                                                                                                                                                                                          35; Conservative
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nes 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 DELSIKNTDNLN
                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                         SEQUENCE FROM N.A.
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                                                      Eukaryota, Alveo
NCBL_TaxID=36329
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                                                                                                                                                                                                                                                       Query Match
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Q8R9Z4
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                                                                                                  --EVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLA 168
                                                                                                                                                                                                                     169 VIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPAC 228
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                                                                                                                                                                                              -----HILSSOIT 174
   YKYDRDLEFIKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKR----HGDDYAKYAE 59
                              RIABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 133; DB 16; Length 39;
Pred. No. 0.0028;
5; Mismatches B; Indels
                                                                                                                                                                               125 TWKKWDEEHKOEFLHAVDARVNELEELLPLIMKDKLLAKGVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein, Complete proteome.
SEQUENCE 39 AA, 4636 WW; EE53CF01F4C1C909 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2033 (TrEMBLrel. 24, Last annotation update)
Expothetical procein HP1590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAYKYDRDLEFIKQLESSDLLDLFEVLVFGKDGEKRHNE 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 23, (TrEMBLrel. 23, 1 (TrEMBLrel. 23, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pylori.";
Nature 388:539-547(1997).
EMBL; AE000656; AAD08629.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     229 IVVATLR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; F64718; F54718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; HP1590; -
                                                                                                                                                                                                                                                                                                                                                                                                                                            026108;
01-JAN-1998
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01-MAR-2003
01-MAR-2003
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RESULT AND THE PART OF THE PAR

51 GDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLJEQ 110

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Last sequence update) Last annotation update)

Created)

QBIANI RESULT 5 Q81AN1 ID Q81AN AC Q81AN DT 01-M DT 01-M

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Indels 105;

W., Yang J.

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SEQUENCE
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                                                                                                                                 ----TLTLFKMGGFKSYQLAVIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWII 207
                                                                                                                                                                          225 FDVKQEFVFFKNEG---KPVSNLTYNSIKKS-------NDPVDRLFR-----QIV 264
                                                                                                                                                                                                                                                                 265 DNVFVAKEKGASSVTVNLKPEİLGKLQISEKSIDGNIVATIVTESEKTKHQIBSNLSLLQ 324
ASDFEKVREKLEVALQ-----GFIKERNFTFKEIAKKISDFLKENFNIELSPEVIER 164
                                                                         ---RLKTQQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 DRRVLAAQIQESLPELHHGHPISMEMVRLVLEGG-----AAIAISSVVRSMVVQQVARQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 FAIRFAGSKLSIAPLVSRGAAMGVARLAVGRSILAFVSTALW----VWFIADLGWQAIST 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNSFASFIKGEG--VLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSLEEMDDE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GRGLSLA-----GNQVLTRILSFLTGPVGWIITGVWTAIDIAGPA--- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKQLESSDLLDLFEVLVFGKDGEKRHN--EKLTSSIEYKRHGDDYAKYABRIAEELQYYG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 LELATEEELODLTBILF----RRELNPLDYLTTPDPIAVQAQDRQAWLDDIBERFRFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 EVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BP-1;
MEDLINE=22255144; PubMed=12240834;
MAKAMURA Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Wakamura Y., Kaneko T., Sato S., Ikeuchi M., Kishida Y., Kiyokawa C., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosyne chococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 102.5; DB 16; Length 276; 19.0%; Pred. No. 7.2; Live 53; Mismatches 111; Indels 49;
                                          111 NM-LSKILERSLEEMDDEEVKEMCDELSIKNTD-----NLNRQALSAA
                                                                                                                                                                                                                                ---VVATL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elongatus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 AA; 31282 MW; D0577A9D97E0CA92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechococcus elongatus (Thermosynechococcus elongatus
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 AA
                                                                                                                                                                                                                         208 IGVWTAEDIAGPAYRVTIPACI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 NYARIIPTIFAIAQIRLIRGEQA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 9:123-130(2002):
EMBL, AP005374; BAC09166.1; --
COMplete proteome.
SEQUENCE 276 AA; 31282 MW;
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23,
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                                                                                                                                                                                                                                                                                                                                                             325 AQLDLKGIKİESV 337
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Best Local Similarity 19.09
Matches 50; Conservative
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8DIH4;
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10801H4
10 04801H4
10 04-M
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RESULT 8 Q8MX30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --BTTLIEON 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     862 PSGGILKESFISTKVYDEILKDPATYLSKVREEYKTLMEDRHILRTEIFPNAENKIVMPV 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROJECT FROM N.A.

RA Dacks J.B., Marinets A., Ford Doolittle W., Cavalier-Smith T.,
Logsdon J.M. Jr.;

RAD Jose S. J.B., Marinets A., Ford Doolittle W., Cavalier-Smith T.,
Logsdon J.M. Jr.;

RAD Jose S. G. RNA Polymerase II Genes from Free-Living Protists:

RT "Analyses of RNA Polymerase II Genes from Free-Living Protists:

RT "Analyses of RNA Polymerase II Cene Spang.";

RNEL, AF395110; AAM45151.1,

BREL, AF395110; AAM45151.1,

GO, GO:0005637; F:DNA-directed RNA polymerase activity; IEA.

GO, GO:0005636; P:Lranscription from Pol II promoter; IEA.

GO, GO:0005636; P:Lranscription, IEA.

GO, GO:0006366; P:Lranscription, IEA.

GO, GO:0006366; P:Lranscription, IEA.

CO, GO:0006366; P:Lranscription, IEA.

BREPPOR INTERPORT IRROGOGE RNA POL RPD1 1.

RICEPPOR IRROGOGE RNA POL RPD1 4.

RICEPPOR IRROGOGE RNA POL RPD1 4.

RICEPPOR IRROGOGE RNA POL RPD1 7.

RICEPPOR IRROGOGE RNA POL RPD1 1.

REAM; PF04991; RNA POL RPD1 1.

REAM; PF04991; RNA POL RPD1 1.

REAM; PF04991; RNA POL RPD1 1.

REAM; PF04991; RNA POL RPD1 1.

REAM; PF04991; RNA POL RPD1 1.

REAM; PF04991; RNA POL RPD1 1.

REAM; PF04991; RNA POL RPD1 7.

REAM; PF04991; R
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NCBI_TaxID=5762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1590 AA; 177446 MW; 5F4C7959D4D77D68 CRC64;
                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNA polymerase II largest subunit (Fragment).
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        1590 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 102; Di
22.8%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021 NCLAQPGEMVGSVAAQSIGEPATQMTL 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TGVWTAIDIAGPAYRVTI 225
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PROSITE; PS00115; RNA POL_II_REPRAT; 7.
NON TER 1590 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                        Naegleria gruberi
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467

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RESULT 9

OBIKG8

A PART TARK TO THE SOLUTION OF

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110 ----QNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNINRQALSAATLTLFKMGGFKS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 DDYKRHKENLEKALIEKGKNNPE------NQNAVEXAQKABKALIEKLNANNY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 DGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDV 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 LOLFEVLVFGKDGEKRENEKLISSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 MDLFVELSEDKDNYKKFYEQFSKNIKLGIHED--AQNRKKLSDMLRYYTSNSNAD----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 MVSLKĠYVSRMKDTQKHIYYITGETKEQVANSSFVERLRKAGLEVIYMIEPIDEYCVQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P., Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A., Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 YQLAVIVANAVAKTILGRGLS--LAGNQVLTRTLSFLTGPVGWIIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GVWTA---IDIAGPAYRVTIPACIVVATLRLKTQQANGDK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618 TMGYMTAKKHLEIN-----PTHPIVETLREKABADKNDK 651
                                                                                                                                                                                                                                                                                                                                              83505 MM; 1A2A962C471CBCF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0E48CF5376BAC48D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 KEYDGKNLVS-VIKEGLELPEDEDEKKKÇEELNTK-FENLCK--
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81;
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Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
EMBL: Ac017147; AAP77543.1;
Hypotherical protein; Complete proteome.
SEQUENCE 556 AA; 61984 MW; 0E48CF5376BAC48D CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
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                                                   GO; GO: 0005224; F:ATP binding; IEA.
GO; GO: 0003754; F:ATP binding; IEA.
GO; GO: 0003754; F:Chaperone activity; IEA.
INCETPC: IPR001364; ATPbind_ATPase.
INCETPC: IPR001404; HSp90.
Pfam; PF02518; HATPase c; 1.
PRINTS; PR00775; HRATSHOCK90.
SMART; SM00387; HATPase c; 1.
PROSTIE; PS00298; HSP90; I.
PROSTIE; PS00298; HSP90; I.
PROSTIE; PS00298; HSP90; II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           7.9%; Score 100.5;
1.6%; Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 99.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 GVLYKEILCDVCDKLKVNYNKKTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE=22709201; PubMed=12810954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  21.6%;
EMBL; U89945; AAB49983.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Conservative
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les 53, Conservative
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                                P07900; 1BYO.
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SEQUENCE FROM N.A.
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01-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 INEY-SHWFNNINDHNKIINKE-----CEELKONNYNTIKEKYERLKEEQEIYIK----- 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 LOYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYN---KKTETTLIEGNNLSKILERSL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, A2014886; AAN37250.1; -. GO, GO, GO, GO, GO, GO, P. P. PROSTIE; F: sugar porter activity; IEA. GO, GO. GOO9401; P: phosphoenolpyruvate-dependent sugar phospho. . .; IEA. InterPro; IPR602114; HPr SerP. S. PROSTIE; PS00589; PTS_HPR_SER; 1. SEQUENCE 1455 AA; 174305 MW; 36PAA1760A898P99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=3D7,
MEDLINE=2255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
Machaer M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Perrea M., Allen J., Salengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraumholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 DRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSI-EYKRHGDDYAKYAERIAEE
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                                                                                                                                                                                            Rhoptry protein, putative.
PF14 0637.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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25.5%; Pred. No. 78;
tive 29; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynchus tschawytscha (Chinook salmon) (King salmon)
                                                                                                                                              Last sequence update)
Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                   FRT; 1455 AA
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                                                                                                                 Created)
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                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                PRELIMINARY;
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Wature 419:498-511(2002)
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292 LIMSFL---AAWVITRL----IVGP
                                                                                                                                                                               PRT;
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Best Local Similarity 24.94
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                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 NTNON 201
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SEQUENCE FROM N.A.
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                     ---IEQNMLSKILERSLEEMDDE---EVKEMCD----E 135
                                                                244 CNRLMCENPRITAVATQSIVASGHIAQAGFSDAIIAALATLANGVIWEVKDMFEGSIDTE 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 KLKVNYNKKTETTLIEGNMLSKILE--RSLEEMDDEE--VKEMCDEL-SIKNTDN---LN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQALSAATLTLFKMGG--FKSY-QLAVIVANAV-----AKTILGRGLSLAGNQVLT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 YKYDRDLEFLKQLESSDLIDLFEVLVFGKDGEKRHNEKLTSS----IEYKRHGDD---- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 ------YAKYAERIAEBLQYYGSNSFASFIKGEG-------VLYKBILCDWCD 93
                                                                                                                                    136 LSI-KNIDNLNRQALSAATLILFKMGGFKSYQLAVIVANAVAKTILGRGLSLAGNQVLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 QASIDQAQAGITKVIGVLFKSADQLS---ANQVSLRIEDVDQARTLLSVML-----VAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633;
                                                                                                                                                                                                                                                                                          LKSIYNGIVSYIKGEVSNLRELLGIILKSLFSAAWVSTLALE 405
                                                                                                                                                                                                                                                  195 TLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLK 237
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PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
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Bacteria; Proteobacteria; Gammapro
Pseudomonadaceae; Pseudomonas.
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                  CDKLKWNYNKKTETEL-
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Best Local Similarity 23.7
Matches 69; Conservative
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57 -----YAERIABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKK----- 102
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--LLETLKLAERVADGD 324
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (32KD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 419:498-511(2002).
EMBL, ABO14829; AAN35246.1; -.
Hypothetical protein.
SEQUENCE 202 AA; 24259 WW; 48FD22A7F21165A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
BC-2 protein (Putative breast adenocarcinoma marker)
                                                                                                                                                                                                                                                                   (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Query Match
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       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLEEMDDEE-----VKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRDLEFLKQLESSDLIDLFEVLVFGK-DGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | : | : | : | : | : : : : | 30 DRERQXLETQEXXIIADIXXONEKQGQMDAVRIMAKDLVRTRRYVRKFVLMRANIQAVSLK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan X., Farmer A.,
"Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] SEQUENCE FROM N.A.
SERAIN=C57BL/61; IISSUE=Cerebellum;
MEDLINE=2108560; FubMed=11217881;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=1009¢;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                               SEQUENCE FROM N.A.

KOCZAR D., Reimer T., Rump A., Merck-Rousseau M.F., Rosenthal

Friese K., Thiesen H.J.;

"Role of the BC-2 gene in breast cancer (in preparation).";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 99; DB 4; Length 222;
21.4%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Indels
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Brain, and Skin;
Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
Obar R.; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03357; SNF7; 1.
SEQUENCE 222 AA; 25104 MW; F2B&6C623829E32E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-070N-2001 (TrEMBLrel. 17, Created)
01-070N-2001 (TrEMBLrel. 17, Last sequence update)
01-070N-2003 (TrEMBLrel. 24, Last annotation update)
1500016111Rik protein (RIKEN oDNA 1500016L11 gene).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Mismatches
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Slater C., Thill G.,
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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es 39; Conserv
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  REPRESENTATIONS OF STATES 
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120 SLBEMDDEE-----VKEMCDELSIKNIDNINRQALSAATLILEKMGGFKSYQLAVIVANA 174
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bromstein M.J., Bult C., Fletcher C., Fujira M., Gartiboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wansaki H., Schoenbach K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 LOYYGS-NSFASFIKG----EGVLYKEILCDVCDKLKVNYNKKIETTLIEQNMLSKILER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 DRDLEFLKQLESSDLLDLFEVLVFGK-DGEKRHNEKLTSSIRYKRHGDDYAKYAERIAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausherg R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AK002267; BAB23919.1; -. EMBL; BC012230; AAH12230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1916203; ISO001611RR.
InterPro; IPR005024; DUF279.
Pfam; PF03357; SNF7; 1.
SRQUENCE 222 AA; 25134 MW; F2B86C623832E29E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 7.7%; Score 99; DB 11; Local Similarity 21.4%; Pred. No. 10; les 39; Conservative 48; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 VA 176
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completed: July 5, 2004, 03:12:04 : 29 Becs

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5, 2004, 03:07:28 ; Search time 16 Seconds (without alignments) 816.336 Million cell updates/sec
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protein search, using sw model
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389414 Total number of hits satisfying chosen parameters: 389414 seqs, 51625971 residues Searched:

Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:\*

1. /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

1. /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

2. /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

4. /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5. /cgn2\_6/ptodata/2/iaa/PGTUS\_COMB.pep:\*

5. /cgn2\_6/ptodata/2/iaa/PGTUS\_COMB.pep:\*

5. /cgn2\_6/ptodata/2/iaa/PGTUS\_COMB.pep:\* 5. 5. .. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00		, e			SUMMARIES	
No.	Score	Match	Length	DB.	QI	Description
	9	28.5	273	4,	9-252-991A-2984	29841,
7	•	Ľ,	321	4	US-09-252-991A-29840	2984
m	24	,	258	4	US-09-489-039A-8852	8852
4	100	,	739	4	US-09-543-681A-6437	
ľ	$\sigma$		222	m		16,
9	99	7.7	274	4	-001C-	5279
7	96	7.5	173	CA	US-08-658-639-12	12,
80	96	7.5	173	m		
0	9	7.4	2125	4	US-09-919-172-29	29, A
10	91.5	7.2	1086	4	-60	7696,
	σ	7.0	281	4	US-09-198-452A-749	
12	-б	7.0	543	4	19-328-352-584	
13	ര		546	4	US-09-345-236B-98	Sequence 98, Appl
14	9	7.0	546	4	19-345-236B-1	
15	89.5	7.0	560	4	US-09-446-301A-50	
16	88.5	9	552	4	US-09-446-301A-4	
17	88.5	6.9	552	4	US-09-099-932-4	
18	88	•	488	4	US-09-489-039A-13363	
19	87.5	6.9	732	7	US-08-533-669A-18	Sequence 18, Appl
20		•	732	4	143-4	4,
21	87.5		732	4	US-09-183-861-18	18,
22	87.5	6.8	732	4	US-09-022-765-18	18,
23	87.5	6.8	732	4	å	8
24	87.5		732	4	-501A-1	18,
25	87.5	6.8	732	4	-206A-	Ę
26	87.5	6.8	732	4	-874-9	ednence
27	87	6.8	491	m	US-09-029-267-2	Sequence 2, Appli

Sequence 3626, Ap	Sequence 27, Appl	Sequence 12, Appl	Sequence 7062, Ap	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 14, Appl	Sequence 21, Appl		Sequence 362, App	Sequence 7, Appli	Sequence 14, Appl	Sequence 21, Appl	Sequence 285, App
US-09-134-001C-3626	US-08-637-670-27	US-09-830-217-12	US-09-107-532A-7062	US-08-719-697-8	US-08-727-616A-8	US-09-481-756-8	US-07-721-775A-2	US-08-339-658-2	US-09-263-933-7	US-09-263-933-14	US-09-263-933-21	US-09-025-769B-265	US-09-025-769B-362	US-09-919-901-7	US-09-919-901-14	US-09-919-901-21	US-09-025-769B-285
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331	528	691	492	264	264	264	286	286	286	286	286	286	286	286	286	286	299
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ALIGNMENTS

KEOULI US-09-25-991A-29841
; Sequence 29841, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEULOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094, 190
PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29841
LENGTH: 273
; TYPE: PRT
: ORGANISM: Pseudomonas aeruqinosa
US-09-252-991A-29841
Onerv Match 28.5%; Score 364; DB 4; Length 273;
Similarity

4 70 SNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSLEEMDDEEV 129 130 KEMCDEL-----SIKNTDNLNRQALSAATLTLFKWGGFKSYQLAVIVANAVAKTIIGRG 183 184 LSLA----GNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQ 239 10 BFLKQLESSDLLDLFEVLVPGKDGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEELQYYG 69 81 28 QILERVSNDDLEPLVEYIL-----KARTESLSKQVDFKRMPEHRRYASAILDELRIFG Gaps 18; 88; Indels 49; Mismatches Conservative 85; Matches a g à ద  $\delta$ à a ેં

RESULT 2
US-09-252-991A-29840
US-08-252-91A-29840, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
A PAPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

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TITLE OF INVENTION:
TITLE OF INVENTION:
WIGHLIGH AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709.1002-001
CURRENT APPLICATION WIGHER: US/09/543,681A
CURRENT FILING DATE: 1090-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 VLFVAATALSFVIGPAM---KGISDAVNKISNQQIRQILKKVLNDGLEAVLGKMIKDIII 622
--LGGPLGAALNSVKA---VSGSAYRVTIPAVLHI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 QYYGSNSFASFIKGEGVLYKBILCDVCDK-----LKVNYNKKTETTL--IEQNMLS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 DRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYABRIAEEL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               623 KALEERLERID----KOLAKEISKKASIMLNRTVVASKLTNSAATNTVNIYGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 100; DB 4; Length 739;
25.6%; Pred. No. 0.089;
tive 42; Mismatches 65; Indels
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ZIP: 0210

ONOPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: ParentIn: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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APPLICANT: KEESER, SUSAN
APPLICANT: OBAR, ROBERT
TITLE OF INVENTION: HATERIALS AND METHODS
TITLE OF INVENTION: HERAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STATE: MA
                                                                                                                                                                                                             ; Sequence 6437, Application US/09543681A; Patent No. 6605709; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/08944604
Patent No. 6218131
  CRGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.61
Matches 54; Conservative
                                                                                                          235 ACLROMIÓ 242
                                                                    232 ATLRLKTQ 239
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ZIP: 02110
                                                                                                                                                                          RESULT 4
US-09-543-681A-6437
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8852
                                                                                                                                                                                                                                                                                                                                                                                                                                    60 RIABELQYYGSNSFASFIK-GEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 RSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NROALSAATLILFKMGGFKSYQLAVIV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 ANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIFACIVV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLK 237
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                                                                                                                                                                                                                                                                                                                                                                                                              1 MAYKYDRDL-BFLKQLESSBLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 YKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSS---IEYKRHGDDYAKYAE
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      AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258;
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                                                                                                                                                                                                                                                                                                                        ; Score 346.5; DB 4;
; Pred. No. 1.1e-28;
42; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Mismatches 100;
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Pred. No. 3.4e-18;
  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIC FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 PRIOR PRICHED DATE: 1998-07-27 NUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 29840

LENGTH: 321
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Patent No. 6610836
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.3%;
                                                                                                                                                                                                                                                                                                                          ch 27.1%;
| Similarity 34.3%;
82; Conservative 42
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Best Local Similarity 28.20
The Total Conservative
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Best Local Similarity
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106 TLIEGNMLSKILERSLE-EMDDEEVKEMCDELSI-KNIDNLNRQALSA---ATLTLFKMG 160
                                           101 NLIKISQANEISRQITNGTMILEBAKYQLEEIYVAKROSSLPFKGIAAAIIATSFLYLQG 160
                                                                                                                        161 GFKSYQLAVIVANAVAKTIIGRGLSLAGNQVLTRTL--SFLTGPVGWIITGVWTAIDIAG 218
                                                                                                                                                            70 SNSFASFIKG----EGVLYKBILCDVCDKLKVNYNKKTETTLIEONMLSKILERSLEEMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEE-----VKEMCDELSIKNTDNINRQALSAATLTLFKWGGPKSYQLAVIVANAVA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 12.2 Application US/08658639
; Patent No. 5944238
; Patent No. 5944238
; Patent No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No. 100 No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.5%; Score 96; DB 2; Best Local Similarity 23.3%; Pred. No. 0.027; Matches 27; Conservative 33; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REGISTRATION NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
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US-08-944-604-12
; Sequence 12, Application US/08944604
; Partent No. 6218131
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           209 HAF---VPSGDLATIIIAAV 225
                                                                                                                                                                                                                                                       219 PAYRVTIP----ACIVVATL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 173 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: REPERENTION: RUDERNIDIS FOR DIAGMOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT PALLICATION NUMBER: 1059-0134,001C
CURRENT FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 LQYYGS-NSFASFIKG----EGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILER 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SLEEMDDEE-----VKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 YKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKT-ET 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --FLILKKFGDEMNKDTIETSREALIKDVVWIAARILLE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 DREROKLETQEKKIIADIKKMAKQGQMDAVRIMAKDLVRTRRYVRKEVLMRANIQAVSLK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 DADLEFLKQLESSDLLDLFEVLVPGK-DGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 99; DB 3; Length 222; Best Local Similarity 21.4%; Pred. No. 0.018; Matches 39; Conservative 48; Mismatches 83; Indels
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   APPLICATE
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOWAS A
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7100
TELEFAX: (617) 248-7100
TELEFAX: (617) 248-7100
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5279, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Staphylococcus epidermidis US-09-134-0012-5279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-944-604-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNYNNDL
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US-09-134-001C-5279
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LENGTH: 274
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Query Match
7.4*; Score 95; DB 4
Best Local Similarity 25.4*; Pred. No. 1.5;
Matches 46; Conservative 35; Mismatches
           Score 95;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 749, Application US/09198452A Patent No. 6559294
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                                                                                                                                                                                                                                                                                                                                                        1163 E 1163
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US-09-543-681A-7696
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US-09-198-452A-749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WI, YING-JYB
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
AJDRESSE: Testa, Hurwitz & Thibeault
STREET: 12 High St.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
7.5%; Score 96; DB 3; Length 173;
Best Local Similarity 23.3%; Pred. No. 0.027;
Matches 27; Conservative 33; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
NOTHER INFORMATION: Incyte ID No. 6673545 3774181CD1
US-03-919-172-29
                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT.INFORMATION:
NAME: MEYERS, ITHOMAS C
REGISTRATION NUMBER: 36,989
REPERENCE/FOOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION:
TELEPHONE: (617) 248-7000
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APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL PROGram
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/09919172
Patent No. 6673545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 173 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                           STATE: M. COUNTRY: ZIP: 021
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
REQ ID NOS: 8344
SEQ ID NOS: 8344
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                                                                                                    2 AYKYDRDLEFLK--QLESSDLLDLF----EVLVFGKDGEKRHNEKLTSSIEYKRHGDDYA 55
                                                                                                                                                                                                                                                          123 EMD-----DEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVI
                                                       38;
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DB 4; Length 2125;
1.5;
                                                                                                                                                                                                                56 KYAERIAEEL--QYYGSNSFASFIKGEG---VLYKEILCDVCDKLKV--
                                                       62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                786 FAYDRGKE-IEÓMO------PETTLIGK--SRAEQEKINA----
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APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan B.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.0004
CURRENT FILIAG DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 98
TENDER OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY FILIAGORY OF THE PROPERTY OF THE P
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APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REPERENCE: 2.1042.0004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 VFEVVGGGPEGDYAAGEEDBVSRNSINFDMASEVQSTDAAKVMELFSALSEEQRNVILMN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 FASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTRILSFLIGPVGWII------TGVWTAIDIAGPAYRVTIPA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 LFEVIUVEGKDGEKRHNEK-----LITSSIEYKRHGDDYAKYAE---RIAEELQYYGSNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.0%; Score 89.5; DB 4; Best Local Similarity 23.5%; Pred. No. 0.75; Matches 60; Conservative 34; Mismatches 92;
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Patent No. 6521454
GENERAL INFORMATION:
APPLICANT: Beonel, James J.
                                                     ; Sequence 98, Application US/09345236B
; Patent No. 6521454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mosquito baculovirus
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; ORGANISM: mosquito baculovirus
US-09-345-236B-121
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Cockburn, Andrew
                                                                                                               APPLICANT: Becnel, James J. APPLICANT: Tukuo, Fukuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tukuo, Fukuda
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US-09-345-236B-121
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH
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US-09-328-352-5845
US-09-328-352-5845

Sequence 5845, Application US/09328352

Patent No. 656258

GENERAL INFCRMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA.

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-66-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 5845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 SLAGN--QVLTRTLSFLTG-----PVGWIITGWWTAIDIAGPAYRVTIPACIVVATL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 DSRDVKVPSLEGKÇTRQEKTTSSKGNTRTESRKFADBEKRVDDEIAEVGSKEBEGESQEF 89
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                                                                                                                                                                                                                                                                                                      Query Match 7.0%; Score 89.5; DB 4; Length 281; Best Local Similarity 22.0%; Pred. No. 0.27; Matches 56; Conservative 49; Mismatches 103; Indels 4
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CURRENT APPLICATION NUMBER: US/09/198,452A
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                            CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 749
LENGTH: 281
                                                                                                                                                                        TYPE: PRT
CRGANISM: Chlamydia pneumoniae
US-09-198-452A-749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLKTQQANGDKKSLQ 249
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US-09-328-352-5845
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Sequence 50, Application US/09446301A

Sequence 50, Application US/09446301A

Patent No. 6506893

Fatent No. 6506893

Fatent No. 6506893

FAPLICANT: EL SOLH, NEVINE

TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED

TITLE OF INVENTION: COMPOUNDER:

TITLE OF INVENTION: COMPOUNDER:

FILE REPRESENCE: 03715-0059

FULRENT APPLICANT APPLICATION NUMBER: US/09/446,301A

CURRENT APPLICANTION NUMBER: US/09/446,301A

KURBER OF SEQ ID NOS: 51

SEQ ID NO 50

LENGTH: 560
                                                                                                                         73 FASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNALSKILERSLEEMDDEEVKEM 132
                                                                                                                                                                                                              243 PENLNDIITDQLRDFMAQELKKAAENYVPKWGSTVGESKSALAITVADRVSRSFWYEGRI 302
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                                                                                                                                                                                                                                                                                                                                                                    186 LAGNOV------LITRILSFLIGPVGWIJ------TGVWTAIDIAGPAXRVIIPA 227
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                                                                                          23 LFEVLVFGKDGEKRHNEK-----LTSSIEYKRHGDDYAKYAE---RIAEELQYYGSNS 72
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                                             92; Indels 69; Gaps
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Query Match 7.0%; Score 89.5; DB 4; Best Local Similarity 23.5%; Pred. No. 0.75; Matches 60; Conservative 34; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :: :: || :|| :| :| :| 435 DIDAVEALB--ELLITYEGVVLFASHDK---
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                                                                                                                                                                                                                                 213 FGAAPSGSGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 CIVVATLRIKTQQAN 242
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US-09-446-301A-50
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US-09-446-301A-50
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US-09-732-091-4 1279 Perfect score:

1 MAYKYDRDLEFLKQLESSDL.....LRLKTQQANGDKKSLQIESI 253 Sequence:

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1586107 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505

Searched:

seq length: 0 seq length: 200000000 Post-processing: Minimum DB Maximum DB

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aae26860 Helicobac	Aae26878 Helicobac	Aaw20486 H. pylori	Aaw24673 H. pylori	Aaw20866 H. pylori	Aae26880 Helicobac	Aae26879 Helicobac	Aaw98774 H. pylori	Aae26876 Helicobac	Aae26873 Helicobac		Aae26874 Helicobac	Aae26872 Helicobac	Aab98720 Human bre	Abp40434 Staphyloc		Abm71523 Staphyloc	Abu48566 Protein e	Abp73563 Candida a	Aaw44365 Breast ca	Aab98717 Human bre	Abu26619 Protein e	Abg77172 Prostate		Abu24813 Protein e
SUMMARIES	ID	AME:26860	AAE26878	AAW20486	AAW24673	AAM20866	AAE26880	AAE26879	AAW98774	AAE26876	AAE26873	AAE26875	AAE26874	AAE26872	AAB98720	ABP40434	ABU15908	ABM71523	ABU48566	ABP73563	AAW44365	AAB98717	ABU26619	ABG77172	ADB79929	ABU24813
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Aag82981 S. epider	Abu19293 Protein e	Aau33755 Staphyloc	Aau36548 Staphyloc	Abp30227 Streptoco	Abp28162 Streptoco	Aag44550 Arabidops	Aag48726 Arabidops	Aag44549 Arabidops	Aag48725 Arabidops	Aag48724 Arabidops	Aag44548 Arabidops	Abp30479 Streptoco	Abp27884 Streptoco	Abr52974 Protein s	Aay51631 M. jannas	Aay52002 M. jannas	Aay31948 Plasmodiu	Aay31947 Plasmodiu	Aag82765 S. epider
AAG82981	ABU19293	AAU33755	AAU36548	ABP30227	ABP28162	AAG44550	AAG48726	AAG44549	AAG48725	AAG48724	AAG44548	ABP30479	ABP27884	ABR52974	AAY51631	AAY52002	AAY31948	AAY31947	AAG82765
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93	93	92.5	92.5	92	92	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	90.5	90.5	90
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# ALIGNMENTS

AAE26860 standard; protein; 253 AA. Helicobacter sp. HP30 protein. (first entry) 13-DEC-2002 AAB26860; AAE26860 

HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.

Helicobacter sp.

W0200251237-A2.

04-JUL-2002.

57-DEC-2001; 2001WO-US048392.

07-DEC-2000; 2000US-00732091.

(ANTE-) ANTEX BIOLOGICS INC.

Jackson WJ; Tian J, Walker R,

WPI; 2002-666854/71.

N-PSDB; AAD44513.

the proteins, useful as vaccines for raising immune response in animals. Movel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding

Claim 1; Page 111-112; 127pp; English.

The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastrilis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is

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disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. PQE/HP30 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                     IAEBLQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTBTTLIEGNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :33 LEEMDDEEVKEMCDELSIKUTDNINRQALSAATLILFKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 GRGLSLAGNQYLTRILSPLIGPYGWIITGVWTAIDIAGPAYRVTIPACIVVATLRKTQQ
                                                                                                                                                                                                                                                                                                                  1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
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                                                                                                                                                                                                                                     Length 265;
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                                                                                                                                                                                                                                       100.0%; Score 1279; DB 5;
100.0%; Pred. No. 1.9e-118;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW20486 standard; protein; 253 AA.
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                                                                                                                                                                                                   Sequence 265 AA;
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01-APR-1996;
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il as vaccines for raising immune response in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                             MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
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                                                                                                                            Gaps
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                                                                                100.0%; Score 1279; DB 5; 100.0%; Pred. No. 1.8e-118;
                                                                                                                          Mismatches
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              Helicobacter sp. HP30 protein
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                                                                                Query Match
Best Local Similarity 100.
Matches 253; Conservative
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N-PSDB; AAD44535.
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AAE2687 RESULT

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N-PSDB; AAT77491
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                  The present sequence is a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypetide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ArCC 5679) was determined from overlapping contigs generated by rechanically shearing the bacterial DNA. The sequences were analysed for OFF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; artisense;
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                                                                                                                                                                                                            99.3%; Score 1270; DB 2; 99.2%; Pred. No. 1.4e-117; ive 1; Mismatches 1;
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Page 651; 1481pp; English.
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This sequence represents an H. pylori cytoplasmic protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for acid sequences, and corresponding proteins, are also useful for meleic acid sequences for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA care blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate tiself easily. The linker-adapter inserts were ligated to each of the 20 pWPX vectors to construct a series of shotgun subclone libraries. The number for this sequence was obtained from the related specification,
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Helicobacter pylori nucleic acid sequences and related proteins - used for diagnostics and therapeutics.
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                                                                                                                              Claim 18; Page 184; 235pp; English
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HP30 plasmid DNA encoded protein
                                                                                                                                                                                                                                                                                                                                                                       Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 jabelçiyesnişpasfikgegvlykeilcdvcdxlkynynkktettliegnmlskillers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSLEYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 IABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGLSLAGNQVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%; Score 1264; DB 5; 98.8%; Pred. No. 5.6e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 126-127; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE26879 standard; protein; 265 AA.
                                                                                                                                                                              07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                               07-DEC-2000; 2000US-00732091.
                                                                                                                                                                                                                                                (ANTE-) ANTEX BIOLOGICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 ANGDKKSLQIESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ANEDKKSLQIESI
                                                                                                                                                                                                                                                                                     Walker R,
                                                                                                                                                                                                                                                                                                                      WPI; 2002-666854/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD44537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 253 AA;
                                                                       Helicobacter sp
                                                                                                                                           04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                     rian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ArCC 5679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HP30; HP56; immune response; therapy; Helicobacter infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLITLFKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIBYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IABELQYYGSNSPASPIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIRYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
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Pred. No. 1.5e-117;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter sp. pQE/HP30 plasmid DNA encoded protein.
                                                                                                                                                                                  BL;
                                                                                                                                                                                                                                                                                                                                          Claim 61; Page 1269; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE26880 standard; protein; 253 AA.
                                                                                                                                                                                  Mellgaerd
                                                                                           95US-00487032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.3%;
                                                          96WO-US009122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGDKKSLQIESI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.2<sup>3</sup>
Matches 251; Conservative
                                                                                                                                                                                  or,
                                                                                                                                                                                  Berglindh
                                                                                                                                                                                                                   WPI; 1997-052306/05.
                                                                                                                                               (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                     N-PSDB; AAT68119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 256 AA;
                                                          06-JUN-1996;
                                                                                             07-JUN-1995;
                                                                                                              01-APR-1996;
                       19-DEC-1996
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                                                                                                                                                                                  Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE26880
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Gaps

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Length 253; Indels 9 9 120 120 240

Helicobacter

EP30;

04-JUL-2002

Tian J,

the

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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYNKKTETTLIEGNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNL---NROALSAATL 154
                                                                                                                             GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 NEKLISSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.9%; Score 472.5; DB 2 63.3%; Pred. No. 1.3e-38; ive 22; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tomb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS. (FUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter sp. HP30-derived peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 1676-1677; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLFKAGGSHSYALAVSVADAMVRQTLG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLFKMGGFKSYQLAVIVANAVAKTILG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE26876 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                              98WO-US006371.
                                                                                                                                                                                                                                                                                                                                                                        97US-00833457,
                                                                                                                                                                                                                                                                                                                                                                                                               97US-00902615.
                                                                                                                                                                                                                                                                                                                                                                                             97US-00881227
                                                                                               H. pylori GHPO 1170 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Al-Garawi A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-542293/46.
N-PSDB; AAX14493.
                                                                                                                                                                                                     Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kleanthous H,
                                                                                                                                                                                                                                                                                                                              01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                        01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1997;
                                                                                                                                                                                                                                              W09843478-A1
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                                                          31-MAR-1999
                                                                                                                                                                                                                                                                                       08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-1997
                 AAN98774;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HP56 plasmid DNA encoded protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LEEMDDEEVKEMCDELSIKNTONINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKWGGFKSYQLAVIVANAVAKTIL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                           type B gastritis, antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 MAYKYDRDLEFLKQLESSDLLDFEVLVFGKDGEKRHNEKLTSSLEYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAEELQYYGSNSFASFIKGEGVLYKEILCDVCDXLKVNYNKKTETTLIEQNMLSKILERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRGLSLAGNOVLTRILSFLIGPVGWIITGVWTAIDIAGPAYFVTIPACIVVATLRLKTQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGISLAGDQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRKTQQ
                                                          Helicobacter infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1264; DB 5; Length 265; Pred. No. 6e-117; 2; Mismatches 1; Indels
                 Helicobacter sp. pQE/HP56 plasmid DNA encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 124-125; 127pp; English
                                                          HP56; immune response; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                     Jackson WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.84;
98.84;
                                                                                                                                                                                                                                                                                         07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                                                                                                                                                   07-DEC-2000; 2000US-00732091.
                                                                                                                                                                                                                                                                                                                                                                        (ANTE-) ANTEX BIOLOGICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.8
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Walker R,
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Oomen RP;

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Gaps

3.

Indels

29; DB 2;

AAW98774 standard; protein; 155 AA.

RESULT 8
AAW98774
ID AAW9

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181

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241

Length 155;

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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
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                                                                                                                                                                                                                 Movel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYAKYAERIAEBLQYYGSNSFASFIKGEGVLYKEILCD 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.5%; Score 198; DB 5; Le
100.0%; Pred. No. 3.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 DYAKYAERIABELQYYGSNSPASFIKGEGVLYKEILCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter sp. HP30-derived peptide #4.
                                                                                                                                                                                                                                                                                       Claim 7; Page 115; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE26875 standard; peptide; 41
                  07-DEC-2000; 2000US-00732091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-2000; 2000US-00732091.
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                                                                 (ANTE-) ANTEX BIOLOGICS INC.
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                                                                                                                                                  WPI; 2002-666854/71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                           Walker R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD44528.
                                                                                                                                                                            N-PSDB; AAD44526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200251237-A2
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                                                                                                           Tian J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                  type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
response; therapy; Helicobacter infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 VGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQANGDKKSLQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQANGDKKSLQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 252; DB 5; Length 49;
Pred. No. 2e-17;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.7%; Scor.
100.0%; Pred. No. zc.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter sp. HP30-derived peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 116; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE26873 standard; peptide; 38
                                                                                                                                                                                                                                                                                                                                                                               Jackson WJ;
                                                                                                                                                                                                                                             07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                                                                                                         07-DEC-2000; 2000US-00732091.
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Best Local Similarity 100.4
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-666854/71.
                                                                                                                                                                                                                                                                                                                                                                               Walker R,
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD44529
                                                                                                             Helicobacter sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200251237-A2.
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                                                                                                                                                                                                                                                                                                                                                                               Tian J,
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RESULT 10 AAE26873

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Gaps 6

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Length 38; Indels

Claim 7; 

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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an liminar ersponse. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcars, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
Page 116; 127pp; English.
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Sequence 41 AA;

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Gaps
                                ö
15.2%; Score 194; DB 5; Length 41; 100.0%; Pred. No. 8.9e-12; tive 0; Mismatches 0; Indels
                                                           145 NROALSAATLTLFKYGGFKSYQLAVIVANAVAKTILGRGLS 185
                                                                               Conservative
                 Local Similarity
                                4.1
 Query Match
                                Matches
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AAE26874 standard; peptide; 30 AA RESULT 12 AAE26874

(first entry) 13-DEC-2002 AAE26874;

Helicobacter sp. HP30-derived peptide #3.

HP30; HF56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer. 

Helicobacter sp.

WO200251237-A2

C4-JUL-2002

07-DEC-2001; 2001WO-US048392.

07-DEC-2000; 2000US-00732091.

(ANTE-) ANTEX BIOLOGICS INC

Jackson WJ

Walker R,

rian J,

WPI; 2002-666854/71 N-PSDB; AAD44527.

Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.

proteins, HP30 and HP56, and nucleic acids encoding

Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcars, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating disorder or disease associated with infection of an animal with Claim 7; Page 115; 127pp; English.

ìs on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence Helicobacter sp. HP30-derived peptide 82888

Sequence 30 AA;

Gaps . 0 Length 30; Indels Score 152; DB 5; I Pred. No. 8.5e-08; 11.94; Scor. 100.04; Pred. No. c. Query Match
Best Local Similarity 100. Matches 30, Conservative

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150 121 LEEMDDEEVKEMCDELSIKNTDNLNRQALS 1 LEEMDDEEVKEMCDELSIKNTDNLNRQALS

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AAE26872 standard; peptide; 30 AA

AAE26872;

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(first entry) 13-DEC-2002 Helicobacter sp. HP30-derived peptide #1.

HP30; HP56; immune response; therapy, Helicobacter infection, vaccine; type B gastritis, antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.

Helicobacter sp.

WO200251237-A2.

04-JUL-2002.

07-DEC-2001; 2001WO-USD48392.

C7-DEC-2000; 2000US-00732091.

(ANTE-) ANTEX BIOLOGICS INC.

Jackson WJ;

Walker R,

Tian J,

WPI; 2002-666854/71. N-PSDB; AAD44525.

Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.

Claim 7; Page 115; 127pp; English

The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an dimmune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastrifs, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or emidical adganosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide

Sequence 30 AA;

Gaps ò Length 30; Indels Score 150; DB 5; I Pred. No. 1.3e-07; ö Mismatches 11.7%; Scor 100.0%; Pred 0; N Conservative Similarity / Ma. Local Sim. 30; Query Match Matches

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1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFG 30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and their use in diagnosing and detecting breast cancer. The breast cancer-associated proteins of the inventor are nuclear matrix proteins cancer-associated proteins of the invention are nuclear matrix proteins designated BC-2 (AAB98721), although 6 other breast cancer-associated conclear matrix proteins (BC-8 (Sequences not given in the specification). The novel conclear matrix proteins (BC-1, BC-3, BC-4, BC-5, BC-6, and BC-7) were nuclear matrix proteins (BC-1, BC-3), BC-4, BC-5, BC-6, and BC-7) were also isolated (sequences not given in the specification). The novel concert cancer calls, but are not present in the nuclear matrix of the breast cancer near proteins are present in the nuclear matrix of the breast cancer diagnosis. The breast cancer matrix of the breast cancer diagnosis. The breast cancer matrix of proteins of the invention or fragments thereof may be detected in a sample of breast tissue or blood from an individual. Isolated breast cancer. Sociated proteins may also be used to prepare antibodies, particularly monoclonal antibodies, which may be used to detect or diagnose breast cancer. Nucleic acids encoding the breast cancer. Or diagnose breast cancer and in the isolation of breast cancer associated proteins of the interact with breast cancer associated proteins. The breast cancer cancer associated breast cancer associated proteins equences which may be used to represent the full-length breast cancer associated proteins. The breast cancer represents the full-length breast cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to novel human breast cancer-associated proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing or detecting breast cancer in an individual comprises detecting the presence of breast cancer-associated proteins in a
                                                                                                                                                                                                                                                                                          Human breast cancer-associated protein; BC-2; marker protein; nuclear matrix protein; diagnosis; detection; tumour.
                                                                                                                                                                                                                                             Human breast cancer-associated protein BC-2, SEQ ID NO:16.
MAYKYDRDLEFLKQLESSDLLDLFEVLVFG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Col 27-30; 30pp; English
                                                                                                             AAB98720 standard; protein; 222
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biological sample.
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                       AAB98720;
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LQYYGS-NSFASFIKG----EGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILER 119 | | | : | : | : | : | : : : | : : : : | DRERQKLETQEKKIIADIKKWAKQGQMDAVRIMAKDLWRTRRYVRKFVLMRANIQAVSLK 89 DRDLBFLKQLESSDLLDLFEVLVFGK-DGEKRHNEKLTSSIEYKRHGDDYAXYAERIAEB 64

12;

Indels

83;

Length 222;

DB 4;

7.7%; Score 99; DB 421.4%; Pred. No. 0.27 tive 48; Mismatches

Query Match Best Local Similarity 21.45 Matches 39; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 SGAEGTRVEDIMARIATKLGYPESNSFVTNTVIEFVLHNEAYPRL-----YRIKIRDT 100
SLEEMDDEE-----VKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANA 174
                                                                                                      epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5279.
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13.8%; Pred. No. 0.37;
ve 44; Mismatches 88; Indels
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                                                                                                                                                                                                                                                                                                                                                        ABP40434 standard; protein; 274 AA.
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                                                                                                                                                                                                                               DA 210
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106 TLIEQNMLSKILERSLE-EMDDBEDVKEMCDELSI-KNIDNLNRQALSA---AILTLERMG 160
101 NLIKISQANEISRQIINGIMILEBEAKYQLEEIXVAKRDSSLPFKGIAAAIIATSFLYLQG 160
  B & B & B &
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<sup>219</sup> PARVTIE----ACIVVAIL 234 209 HAF---VPSGDLATIIIAAV 225

Search completed: July 5, 2004, 03:11:25 Job time : 40 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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model š protein search, using OM protein Run on:

5, 2004, 03:10:43 ; Search time 14 Seconds (without alignments) 1738.318 Million cell updates/sec

US-09-732-091-4 1279 Title: Perfect sc Sequence:

score:

1 MAYKYDRDLEFLKQLESSDL.....LRLKTQQANGDKKSLQIESI 253

, Gapext 0.5 BLOSUM62 Gapop 10.0 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 of hits satisfying chosen parameters: Total number

seg length: 0 seg length: 2000000000 Minimum DB : Maximum DB :

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 78:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	probable oxidoredu	probable oxidoredu	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet		probable ATP /GTP	probable preprotei	8-amino-7-oxononan	hypothetical prote	probable permease	abortive phage res	hypothetical prote	bullous pemphigoid	penicillin amidase	transposase ISC122	exodeoxyribonuclea	hypothetical prote	E	-	hypothetical prote
		D64718	B71800	E64718	A71800	C64718	C64721	AC0503	C90630	CB5481	F64718	C89910	AE0360	G90546	C81380	A81385	E71330	G70355	T33071	F96920	A47025	C81327	A40937	S49252	E90488	G70178	T33070	I39665	T16536	H81345
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repeat organellar	RNA polymerase sig	PET112 homolog - M	hypothetical prote	rad 26 protein - f	probable membrane	replication factor	body-wall muscle t	hypothetical prote	hypothetical prote	vsaa-like (mycopla	hypothetical prote	hypothetical prote	ribonucleoprotein	conserved hypothet	CT671 hypothetical
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7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.1	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0
92	91.5	91.5	91.5	91.5	91.5	91.5	91	91	90.5	90.5	90.5	90.5	90	89.5	89.5

RESULT 1 D64718 D64718 Conserved hypothetical protein HP1588 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999 C;Accession: D64718 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKerson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,

Aguine 388, 539-547, 1997

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A.Accession: D64718
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Status: Jreliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-253 < TOM>
A.Cross-references: GB:AE000656; GB:AE000511; NID:g2314771; PIDN:AAD08627.1; PID:g2314

ò 1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER 60 Gaps ô Query Match 100.0%; Score 1279; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 4e-88; Matches 253; Conservative 0; Mismatches 0; Indels 0 ò

120 9 61 IAEELQYYGSNSPASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 셤 à

61 IARELQYYGSNSFASFIKGBGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 120 121 LEEMDDEEVKEMCDELSIKKTDNINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180 g ð

121 LEEMDDEEVKEMCDELSIKATDNINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180 240 181 GRGLSLAGNQVLTRTLSPLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 240 181 GRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 셤 à

253 241 ANGDKKSLQIESI 253 241 ANGDKKSLQIBSI Š 셤

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RESULT 2

B71800

hypothetical protein jhp1494 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999
C;Accession: B71800
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R

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Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cispecies: Obstage 1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cisture: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cispecies: Obstage 1997 #sequence_revision 0.2 Accession: C64718
Richardson, J.D.; Kalley, J.M.; Cotton, M.D.; Weidman, J.M.; Fulli, C.; Bowman, C.; Watthey, Nature 188, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A.Reference number: A64520; MUID:97394467; PMID:925185
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Reference DNA
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hypothetical protein jhp1493 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 12-Feb-1999 #sequence_revision 0.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. I. Jane, C., Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
Nature 397, 176-180, 1999
A;Teference number: A71800
A;Reference number: A71800
A;Status: preliminary
A;Status: preliminary
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Best Local Similarity 59.8%; Pred. No. 7.4e-40;
Matches 122; Conservative 32; Mismatches 46;
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Pred. No. 2.8e-28;
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                                                                                                                                                                                               207
                                                                                                                                                                   181 YRVTIPACILVATLRLKA-QANEIKNIL
                                                                                                                       221 YRVTIPACIVVATLRLKTQQANGDKKSL
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A;Residues: 1-209 <ARN>
A;Cross-references: GB:AE001571; G
A;Experimental source: strain J99
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Best Local Similarity
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A,Gene: jhp1493
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ilves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A.Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Accession: B71800
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-253 cARN>
A; Residues: 1-253 cARN>
A; Cross-references: GB:AE001571; GB:AE001439; NID:G4156120; PIDN:AAD07073.1; PID:G415612
A; Cross-references: GB:AE001571; A; Cross-references: GB:AE001571; A; Cross-references: GB:AE001571; GB:AE001439; NID:G4156120; PIDN:AAD07073.1; PID:G415612
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A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karzk, P.D.; Smith, H.O.; Fraser, C. A; Reference number: A64520; MUID:97394467; PMID:9252185
A; Accession: E64718
A; Molecule type: DNA
A; Seatules: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-207 < TOM>A; A; Coss. references: GB:AE000511; TIGR:HP1589
C; Genetics:
A; Start codon: TTG
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C,Species: Helicobacter pylori
C,Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Aug-1997
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Pred. No. 1.9e-87;
L; Mismatches 1;
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Matches 251;
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Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0
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-LIST=45 -DOCALIGN=200 -TRR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15
-MODE=LOCAL -UUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000;
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-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-PROFILE - TARROUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGAPPEXT=0.5 -FGAPOP=6
-PROFILE - TARROUT=10 -WARN TIMEOUT=0.5 -DELOP=6 -DELEXT=7 Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aae26860 Helicobac	Aae26878 Helicobac	Aaw20486 H. pylori	Aaw24673 H. pylori	Aaw20866 H. pylori	Aae26880 Helicobac	Aae26879 Helicobac	Aaw98774 H. pylori	Aae26876 Helicobac	Aae26873 Helicobac
SUMMARIES		ID	AAE26860	AAE26878	AAW20486	AAN24673	AAW20866	AAE26880	AAE26879	AAW98774	AAE26876	AAE26873
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Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.

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# ALIGNMENTS

HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer. AAE26860 standard; protein; 253 AA Jackson WJ; Helicobacter sp. HP30 protein. 07-DEC-2001; 2001WO-US048392. 37-DEC-2000; 2000US-00732091. (ANTE-) ANTEX BIOLOGICS INC. (first entry) WPI; 2002-666854/71. Tian J, Walker R, N-PSDB; AAD44513. Helicobacter sp. WO200251237-A2. 04-JUL-2002. 13-DEC-2002 AAE26860; RESULT 1 

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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastrits, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. PQE/HP30 protein
Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                                                                                                                                                                                                                                 HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                                                                                                                                       AAE26878 standard; protein; 265
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                                                                                                                                                                                                                        (first entry)
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N-PSDB; AAD44535.
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                                                The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, wirulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30 protein
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         TIGGATTICITIGAGGIGCITCITITIGGIAAAGACGGCGAAAAAAGACACAAAAAA
                                            LeuaspleuPheGluValLeuValPheGlyLysAspGlyGluLysArgHisAsnGluVs
                                                                    CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTAOGCTAAATACGCAGAAAGA
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The present sequence is a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori infe cycle activators or inhibitors. The genomic sequence of H. pylori (ARCC 5679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for open teast 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts

Length: Matches: L Mismatches: Indels:

6.94e-134 1270.00 99.60% 99.21%

Sequence 253 AA;

Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vactimes to treat or prevent H. pylori infection, and to detect Helicobacter.

61; Page 651; 1481pp; English

Claim

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Smith

(ASTR ) ASTRA 07-JUN-1995; 01-APR-1996;

WPI; 1997-052306/05. N-PSDB; AAT67811.

95US-00487032 96US-00630405

ACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCGACTTTAAACGCTGTTTAAAATGGGG LeuThrSerSerIleGluTyrLysArgHisGlyAspAspTyrAlaLysTyrAlaGluArg ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC TTGGAAGAATTGATGATGAAGAAGTGAAAGAAATTGTGCGATGAATTATCCATAAAAAAC ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA TIGGATITIGITIGAGGIGCITGITITIGGTAAAGACGGCGAAAAAAGACACAATGAAAAA CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA 19 :4 21 121 41 181 81 301 101 361 121 421 241 셤 යු 셤 g g à 유 8 Š ò g ò 8 Š ₽

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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; ducdenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori

06-JUN-1996;

19-DEC-1996

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H. pylori cytoplasmic protein, 4095342.aa

(first entry)

29-JJL-1997

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standard; protein;

AAW20486

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents an H. pylori cytoplasmic protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Autisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMpX vectors, while the overhang is not self-complementary. Therefore
                                                                                                                                                                                                                                                                                                                                                                    Transmembrane, cytoplasmic; cell envelope, flagella, transport; secreted, periplasmic; chronic gastritis, duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine, immunise; detection; antisense; inhibition.
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                                                                                  TATAGGGTAACCATACCGGCATGCATTGTGGTTGCCACTTTACGCCTAAAAACACAGCAA
ThrispashLeuAshArgGlnAlaLeuSerAlaAlaThrLeuThrLeuPheLysMetGly
                        GGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTA
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                                                                                                                                                                                                                             AlaAsnGluAspLysLysSerLeuGlnIleGluSerVal 253
                                                                                                                                                                                                               GCCAATGGAGATAAGAAGTCGTTGCAAATAGAATCCATT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequences and
                                                                                                                                                                                                                                                                                                                                                        H. pylori cytoplasmic protein, 4095342.aa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutics.
                                                                                                                                                                                                                                                                                     AAW24673 standard; protein; 253
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for diagnostics and
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N-PSDB; AAT77491.
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the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pWPX vectors to construct a series of shotgun subclone libraries. The purified DNA samples were then sequenced. Note: The ORF/protein reference number for this sequence was obtained from the related specification, W09640893
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                                                                                                                                                                                                                                                                                                                                                                        TTGGATTTGTTTTGAGGTGCTTGTTTTTGGTAAAGACGGCGAAAAAAGACACAATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                        CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGTCTTATACAAAGAGATTTTATGCGATGTGCGATAAATTAAAGGTCAATTACAAC
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                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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1270.00
99.60%
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Best Local Similarity:
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GGTCCTGTTGGCTGGATCATTACAGGCGTATGGACGATTGATATTGCAGGGCCGGCT 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis, antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                                                                                                                                                                                                                241 GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC
                                                                                                                GOGCGTGGTTTATCGCTTGCGGCCAATCAGGTGCTTACAAGAACTCTGAGCTTTTTAACA
44 LeuThrSerSerIleGluTyrLysArgHisGlyAspAspTyrAlaLysTyrAlaGluArg
                                  ATCGCTGAAGAGTTGCAATACTATGGCAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
                                                   64 IlealaGluGluLeuGlnTyrTyrGlySerAsnSerPheAlaSerPheIleLysGlyGlu
                                                                                                                                                                 TTGGAAGAATTGGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAC
                                                                                                                                                                                                                                                                                               421 ACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCGACTTTAACGCTTTTAAAATGGCG
                                                                                                                                                                                                                                                                                                                                                               GGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 AlaAsnGluAspLysLysSerLeuGlnIleGluSerVal
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N-PSDB; AAD44537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ARCC 56679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for DR omputer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
                                                                                                                                      Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                       H. pylori cytoplasmic protein, 12ge20305orf30.
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             Ā
             standard; protein; 256
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96US-00630405.
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99.60%
99.21%
94.14%
                                                                            (first entry)
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                                                                                                                                                                                                                             Helicobacter pylori.
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Best Local Similari
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01-APR-1996;
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Pred. No.:
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                                            AAW20866;
               AAW20866
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GlyProValGlyTrp1lelleThrGlyValTrpThrAlalleAsp1leAlaGlyProAla 220
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1264.00
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93.70%
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                                                               The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmacoutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcars, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of the incobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HP30 plasmid DNA encoded protein
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               bl Helicobacter proteins, HP30 and HP56, and nucleic acids encoding proteins, useful as vaccines for raising immune response in animals
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Conservative:
Mismatches:
Indels:
                                                  English.
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                                                                                                                                                                                                                                                                                                                          (1-253)
                                                   Disclosure; Page 126-127; 127pp;
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                                                                                                                                                                                                                                               3.3e-133
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99.60%
98.81%
93.70%
                     Novel Helicobacter
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Best Local Similarity:
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with telicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastrif cancers such as adenocarcinoma, and low grade B peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of the phicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HP56 plasmid DNA encoded protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                  221 TyrargValThrIleProAlaCysIleValValAlaThrLeuArgLeuLysThrGlnGln
TATAGGGTAACCATACCGGCATGCATTGTGGTTGCCACTTTACGCCTAAAAACACAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter sp. pQE/HP56 plasmid DNA encoded protein.
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112 AATGAAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATAC 171
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                                                                                                                                         New isolated Helicobacter polynucleotides - used to develop products for
the diagnosis, prevention and treatment of Helicobacter infections and
gastrointestinal diseases.
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MetValArgGlnThrLeuGly
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97US-00881227
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78.23$
63.27$
35.03$
                                                                               Al-Garawi A,
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N-PSDB; AAX14493.
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                                                                                                                                                                                                                                                                                                                                             Sequence 155 AA;
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                                                                               Kleanthous H,
24-JUN-1997;
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                                                                                             CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA
                                                                                                             LeuThrSerSerLeuGluTyrLysArgHisGlyAspAspTyrAlaLysTyrAlaGluArg
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               MetAlaTyrLysTyrAspArgAspLeuGluPheLeuLysGlnLeuGluSerSerAspLeu
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Helicobacter infection; gastroduodenal disease;
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                                                                                              HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis, antichinflammacory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; annibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 TTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAGATTTTATGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheAlaSerPheIleLysGlyGlyGlyValLeuTyrLysGluIleLeuCysAsp
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                                                                                                       sp. HP30-derived peptide #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 115; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jackson WJ;
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                                                                                                                                                                                                                                                              Helicobacter sp.
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                                                                                                       Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIAACCATACCGGCATGCATTGTGGTTGCCACTTTACGCCTAAAAACACAGGAAGCCAAT 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  il Helicobacter proteins, HP30 and HP56, and nucleic acids encoding proteins, useful as vaccines for raising immune response in animals.
                                                                                                                            HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                                                                    Helicobacter sp. HP30-derived peptide #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
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N-PSDB; AAD44529.
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphona. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
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                                                                                             HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                                            Helicobacter sp. HP30-derived peptide #3.
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                                                                                                                                                                                                       Helicobacter sp.
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                                                                           E230; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lympioma; virulence; antibacterial; gastric cancer; immunostimmlant; cytostatic; peptic ulcer.
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                                       sp. HP30-derived peptide #4.
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                                                                                                                                                                                 Helicobacter sp
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                                       Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 LysPheValLeuMetArgalaAsnIleGlnAlaValSerLeuLys--IleGlnThrLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 ysserAsnAsnSerMetAlaGlnAlaMetLysGlyValThrLysAlaMetGlyThrMetA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 ACAAAGAGAITITIAIGCGAIGIGCGAIAAAITAAAGGICAAITACAACAAGAAAACIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TrpProSerLysAlaArgTrpMetLeuPheAlaSerTrp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGC---AATAGTTTTGCGAGTTTCATTAAAGGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-732-091-3 (1-759)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B ell lymphoma. The invention is useful as reagents for clinical or
                              HP30, HP56; immune response; therapy, Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast cancer-associated protein; nuclear matrix protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast cancer-associated protein fragment BC-2 SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000000
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITGGATTTGTTTGAGGTGCTTGTTTTTGGT 90
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Helicobacter sp. HP30-derived peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-30)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 115; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW44365 standard; peptide; 173
                                                                                                                                                                                                                                                                                                                           Jackson WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-732-091-3 (1-759) x AAE26872
                                                                                                                                                                                                                         07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                                                                         07-DEC-2000; 2000US-00732091.
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100.00%
11.12%
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                                                                                                                                                                                                                                                                                                                                                            2002-666854/71
                                                                                                                                                                                                                                                                                                                           Walker R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity:
                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD44525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30 AA;
                                                                                                                                                    WO200251237-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                           Tian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
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-----GAAGGAGTCTTAI 250

85

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à 셤 45

25

---GlnLyeThrTrpValAlaProGlyTyrValArg

173 41 37 72 29 5

Conservative: Mismatches: Indels:

101.50 43.58% 22.91% 7.52%

x AAW44365 (1-173)

Length: Matches:

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The present sequence represents a breast cancer-associated protein fragment for use in a method for diagnosing breast cancer in tissue or body fluid by detecting one or more breast cancer-associated protein(s). Alternatively a nucleic acid encoding a breast cancer-associated protein is detected in the sample by the use of a nucleic acid probe. The breast cancer-associated protein is detected in the sample by the use of a nucleic acid probe. The breast cancer-associated proteins, encoding nucleic acids and antibodies are useful in diagnostic assays and kits for breast cancer detection. The proteins are also useful in screening for inhibitory compounds and monitoring effectiveness of treatments. The antibody, or pharmacoutical compositions containing the antibody or the inhibitory compound, can be administered to patients to treat breast cancer. The methods allow reliable and early diagnosis of breast cancer, or prediction of its but not in non-cancerous breast cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing breast cancer by detecting a breast cancer-associated protein - allows early and reliable diagnosis and treatment monitoring, and antibody or inhibitory compounds useful for treating breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 32; 47pp; English
detection; diagnosis; antibody.
                                                                                                                                                                                                                                                                                                                                                               97WO-US009529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00658639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu Y:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-042336/04.
N-PSDB; AAV15304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keesee SK, Obar R,
                                                                                          Homo sapiens
                                                                                                                                                                               WO9746884-A1
                                                                                                                                                                                                                                                                                                                                                               03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1996;
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Conservative: Mismatches: Indels: Length: Matches:

0.0325 101.50 43.58% 22.91% 7.52%

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

Sequence 173 AA;

Alignment Scores: Pred. No.:

Score:

Gaps:

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-----GTGAAAGAAATGTGCGATGAATTATCCATAA 415
                                                                                                                               inlleMetAspMetLysGluGluMetMetAsnAspAlaIleAspAspAlaMetGlyAspG 105
                                                                                                                                                                                                                                                                  125 erLeuThrAspGluLeuSerAsnLeuProSerThrGlyGlySerLeuSerVal---AlaA 144
                                                                                                                                                                                                             416 AAAACACGGACAATTTAAAACAGACAAGCCTTAAGCGCGGGCGACTTTAACGCTGTTTAAAA
                                                                                                                                                                                                                                                                                                                                                                Human breast cancer-associated protein BC-2 portion, SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing or detecting breast cancer in an individual comprises detecting the presence of breast cancer-associated proteins in a biological sample.
                                                                                                                                                                                                                                                                                                                              TGGGGGGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast cancer-associated protein, BC-2, marker protein, nuclear matrix protein, diagnosis, detection, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Col 21-24; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB98717 standard; protein; 173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00944604.
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                                                                                             371 TGGATGATGAAGAA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-396355/42.
N-PSDB; AAH25091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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AAB9 8717

AAB9 8717

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Job time : 69 secs The invention relates to novel human breast cancer-associated proteins, and their use in diagnosing and detecting breast cancer. The breast cancer—associated proteins of the invention are nuclear matrix proteins (cancer—associated proteins of the invention are nuclear matrix proteins (soform B (BC-8B, AAB98722), although G other breast cancer—associated nuclear matrix proteins (BC-1, BC-3, BC-4, BC-5, BC-6, and BC-7) were nuclear matrix proteins (BC-1, BC-3), BC-4, BC-5, BC-6, and BC-7) were nuclear matrix proteins (BC-1) are specification). The novel breast cancer—associated proteins are present in the nuclear matrix of breast cancer cells, but are not present in the nuclear matrix of the breast cancer associated proteins (AAB98709-AAB98716), and methods for their use in breast cancer diagnosis. The breast cancer marker proteins of the invention or fragments thereof may be detected in a proteins of breast tissue or blood from an individual. Isolated breast cancer—associated proteins may also be used to prepare antibodies, particularly monoclonal antibodies, which may be used to detect or diagnose breast cancer. Nucleic acids encoding the breast cancer-associated proteins may also be used in the diagnosis and detection of breast cancer, and in the isolation of DNA or protein sequences which may interact with breast cancer-associated nuclear matrix proteins. The present sequence represents a portion of breast cancer-associated protein BC-2 referred to in an exemplification of the invention

-60-SD	US-09-732-091-3 (1-759) x AAB98717 (1-173)
ò	26 TGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTGGATTTGTTTG
qa	2 TrpProSerLysAlaArgTrpMetLeuPheAlaSerTrp 14
λõ	86 TIGGIAAAGACGGCGAAAAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAAA 145
qa	15GlnLysThrTrpValAlaProGlyTyrValArg 25
λō	146 GGCATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATG 205
q	26 LysPheValLeuMetArgalaAsnIleGlnAlaValSerLeuLysIleGlnThrLeuL 45
ò	206 GGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTAT 250
qa	45 ysSerAsnAsnSerMetAlaGlnAlaMetLysGlyValThrLysAlaMetGlyThrMetA 65
č	251 ACAAAGAGATTITAIGCGAIGTGCGGTAAAITAAAGGTCAATTACAACAAGAAAACTG 310
쉱	65 snarg3lnLeuLysLeuProGlnIleGlnLysIleMetMetGluPheGluArgGlnAlad 85
ζō	311 AAACGACTTTAATTGAACAAAACATGCTTTCTAAAATCTTAGAAAGATTTGGAAGAAA 370
Ą	85 lulleMetAspMetLysGluGluMetMetAsnAspAlaileAspAspAlaMetGlyAspG 105
ζŏ	371 IGGAIGAAGAAGIGAAAGAAATGIGCGAIGAAITAICCAIAA 415
ą	:::               ::::
λō	416 AAAACACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAA 475
q	125 erLeuThrAspGluLeuSerAsnLeuProSerThrGlyGlySerLeuSerValAlaA 144
Š	476 TGGGGGGTTTTAAATCTTATCAATTAGCTGTCATTGCGAATGCGGTCGCA 528
qq	144 laGlyGlyLysLysAlaGluAlaAlaAlaSerAlaLeuAlaAspAlaAspAla 161
Search	Search completed: July 5, 2004, 03:03:13

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(without alignments) 6489.722 Million cell updates/sec
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                                                                                                    ; Search time 22.5 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                     OM nucleic - protein search, using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

1: pirl:\* 2: pirl:\* 3: pir3:\* 4: pir4:\* Database

Pred. Mo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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hypothetical prote conserved hypothet probable D-2-hydro	probable ATP /GTP	hypothetical prote	8-amino-7-oxononan	hypothetical prote	probable permease	abortive phage res	hypothetical prote	bullons pemphigoid	hypothetical prote	penicillin amidase	transposase ISC122	exodeoxyribonuclea	hypothetical prote	penicillin amidase	hypothetical prote	hypothetical prote	repeat organellar	RNA polymerase sig	PETII2 homolog - M	hypothetical prote	rad 26 protein - f	probable membrane	replication factor	body-wall muscle t		hypothetical prote	transposase-like p
AE0360 G90546	A81385	A70144 E71330	G70355	T33071	F96920	A47025	C81327	A40937	A86302	549252	E90488	G70178	T33070	I39665	T16536	H81345	T18372	G72253	A64320	T24622	S42797	S53378	E64477	A45488	AI2368	B97214	E64571
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98	97.5	97	96.5	96	96	95.5	95	95	94.5	93.5	93	93	92.5	92.5	92.5	92	92	91.5	91.5	91.5	91.5	91.5	91.5	91	91	90.5	90.5
15	18	0 19	2.7	22	23	24	25	26	27	28	29	30	31	32	33	ን የ	35	36	37	œ M	ØΕ	40	41	42	43	44	45

conserved hypothetical protein HP1588 - Helicobacter pylori (strain 26695) (Species: Helicobacter pylori C;Species: 99-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999

C. Accession: D64718

C. Accession: D64718

C. Accession: D64718

Fromb, J.F.; Whatte, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Fromb, J.F.; Whatte, O.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MuID:97394467; PMID:9252185
A; Accession: D64718
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-253 < TOM>A; Cross-references: GB:AE000656; GB:AE000511; NID:92314771; PIDN:AAD08627.1; PID:92314

Length:
Matches:
Conservative:
Mismatches:
Indels: 1.5e-97 1279.00 100.00% 100.00% 94.81% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores: Pred. No.: Score: 7

US-09-732-091-3 (1-759) x D64718 (1-253)

Oy 1 AIGGCATACAAATAIGATAGACACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA 60
Qy 61 TIGGAITIGITIGAGGIGCITIGITITIGGIAAAGACGGCGAAAAAGACAATGAAAAA 120

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C; Species: Helicobacter pylori
C; Decies: Helicobacter pylori
C; Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Aug-1997
C; Accession: E64718
R; Tomb, J.F; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loffus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKeison, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A, Authors: Wallin, B.; Hayes, W.S.; Bordovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A, Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A, Reference number: A64520; MUID:97394467; PMID:9252185
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C;Genetics:
A;Start codon: TTG
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C; Parett 2
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C; Paretty: strain J999
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C; Accession: B71800
B; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUD: 99120557; PMID: 9923682
A; Molecule type: DNA
A; Residues: 1-253 *ARN>
A; Cross-references: GB.AE001571; GB.AE001439; NID: 94156120; PIDN: AAD07073.1; PID: 9415612
C; Genetics:
A; Generics: strain J99
C; Genetics: A; Generics: strain J99
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IlealadluLeuclnTyrTyrGlySerAsnSerPheAlaSerPheIleLysGlyGlu
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                                           ATCGCTGAAGACTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
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                 21 LeuaspLeuPheGluValLeuValPheGlyLysAspGlyGluLysArgfisAsnGluLys
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 ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA
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RESULT 3
(E64718)
Conserved hypothetical protein HP1589 - Helicobacter pylori (strain 26695)

A;Status; preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-207 <TOM>

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Conserved hypothetical protein HPIS87 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
R;Tomb, J.F.; Sutton, G.G.; Fleischmann, R.
Fetremon, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKerson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
N;Reference number: A64520; MUID:97394467; PMID:9252185
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Retersion: Cf4718
A;Rolecule type: DNA
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                     A;Gene: jhp1493
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Mypotherical protein jhp1493 - Helicobacter pylori (strain J99)

C,Species: Helicobacter pylori

C,Bacession: A71800

C,Bacession: A71800

C,Accession: A71800

C,Accession: A71800

Mylo:99120557; PMID:9923682

A;Reference number: A71800

A;Reference number: 
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Matches:
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C;Species: Escherichia coli
C;Species: Escherichia coli
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: C64721; D56688; Z38462
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rselence 277, 1453-1462, 1997
A;Trile: The complete genome sequence of Escherichia coli:K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64721
A;Steatus: nucleic acid sequence not shown; translation not shown
A;Molecule Type: DNA
A;Cression: C64721
A;Steatus: nucleic acid sequence not shown; translation not shown
A;Molecule Type: DNA
A;Cross-references: GB:AECOULZ; GB:U00096; NID:91786192; PIDN:AAC73122.1; PID:91786193;
A;Experimental source: strain K-12, substrain MG1655
B;James, R; Dean, D.O.; Debbage, J.
DNA Seq. 3, 327-332, 1993
A;Title: Five open reading frames upstream of the dnak gene of Escherichia coli.
A;Reference number: A56688; MUID:94003405; PMID:8400364
               A; Cross-references: GB: AE000656; GB: AE000511; NID: 92314771; PIDN: AAD08626.1; PID: 9231477
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A;Cross-references: GB:X67700; NID:g41754; PIDN:CAA47934.1; PID:g41759
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ThrTrpLysLysMetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg 144
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    serov
  Salmonella enterica
A,Title: Complete genome sequence of a multiple drug resistant Salmonella enter A,Reference number: ABC502; MUID:21534947; PMID:11677608
A,A,Rocession: AC0503
A,Status: preliminary
A,Rolecule type: DNA
A,Residues: 1-237 <PRA>
A,Residues: 1-237 <PRA>
A,Cross-references: GB:AL513382; PIDN:CAD01163.1; PID:g16501293; GSPDB:GN00176
C,Genetics:
A,Gene: STY0010
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||| :::salaspalaLysValSerGiuLeuGluGluLeuLeuProLeuLeuMetLysAsparg 159
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40
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Matches:
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265.00
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substra
probable oxidoreductase ECSD012 [imported] - Escherichia coli (strain 0157:H7, substicispecies: Bscherichia coli
C;Species: Bscherichia coli
C;Daces: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: C90630
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, (gasawara, N.; Yasunagay, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001
A;Reference number: A99629; MUD:21156231; PMID:11258796
A;Accession: C90630
A;Accession: C90630
A;Molecule type: DNA
                                                                                                                                                                                                                                                                      A;Residues: 1-237 <HAY>
A;Residues: 1-237 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33434.1; PID:g13359467; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics: A;Gene: ECS0012
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ThrTrpLysLysMetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg
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| ArgileLeuArgThrHisAlaAlaMetSerValLeuGlyHisGlyLeu---LeuArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 AGAATOGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTAC
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165 ValSer----
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Query Match:
DB:
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Oy 505 GTCATTGTTGCGAATGCGGTGGAAAACCATTCTAGGGGGTTGATTGGCTTGCGGGC 564        :::	825 206 206 885 223 8ULT 10 4718 Pothetical E Species Hel Species Hel Accession: B Accession: F Accession: A Accession: A A Accession: A A Accession: A A A A A A A A A A A A A A A A A A A	Nature 388, 539-547, 1997 A;Authors: Wallin, E., Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Authors: Wallin, E., Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185 A;Accession: E64718 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-39 <tom> A;Residues: 1-39 <tom> A;CCcss-references: GB:AE000656; GB:AE000511; NID:92314771; PIDN:AAD08629.1; PID:9231</tom></tom>	Alignment Scores:  Pred. No.:  Score:  Score:  133.00  Matches:  Score:  Pred. No.:  133.00  Matches:  Conservative: 5  Best Local Similarity:  9.86\$  Mismatches:  Caps:  0  Caps:  0  1 ATGGATACAAATAGAAATAGAAATTTTAAAGCAATTGGAATTA 60	Db 1 MetalaTyrargTyragpSerAspLeuGluPheLeuLysArgLeuSerSerSerAspLeu 20  Qy 61 TTGGATTTGTTTGAGGTGCTTGTTTTTGGTAAAGAGGGGGAAAAAAGACACAATGAA 117  Db 21 LysAspLeuPheAspAlaLeuValTyrAspGluAspGlyThrLeuArgMetAsnGlu 39	RESULT 11 D90630 hypothetical protein ECs0011 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Bscherichia coli C;Species: Bscherichia coli C;Decies: Bscherichia coli C;Decies: Bscherichia coli C;Decies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: 190630 R;Hayashi, T.; Makino, K.; Chnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA, Res. B, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gi, A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90630 A;Accession: D90630 A;Accession: D00630 A;Accession: DNA A;Molecule type: DNA A;Accession: Coli c, C, C, C, C, C, C, C, C, C, C, C, C, C,
Oy 625 GGCGTATGGACTGATATTGCAGGGCGGCTTATAGGGTAACCATACCGGCATGC 684	BSULT 9  8481  Solur 9  85481  Cobable oxidoreductase Z0011 [imported] - Escherichia coli (strain O157:H7, substrain E Species: Escherichia coli Species: Escherichia coli Species: Escherichia coli Species: L6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 Accession: C85481  Stricte: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  Recession: C85481  Status: preliminary Residues: L7297 c870> Cross-references: GB:AE005174; NID:g12512689; PIDN:AAG54311.1; GSPDB:GN00145; UMGP:Z00  Cross-references: GB:AE005174; NID:g12512689; PIDN:AAG54311.1; GSPDB:GN00145; UMGP:Z00  Gross-references: GB:AE005174; NID:g12512689; PIDN:AAG54311.1; GSPDB:GN00145; UMGP:Z00  Gross-references: GB:AE005174; NID:g12512689; PIDN:AAG54311.1; GSPDB:GN00145; UMGP:Z00  Gross-references: GB:AE005174; Substrain EDL933	11   Cores: 8.69e-14 Length: 237 262.00 Matches: 76   Ilarity: 48.99\$ Conservative: 45   Similarity: 30.77\$ Mismatches: 36   Is.42\$ Indels: 6	OS-09-732-091-3 (1-759) x C85481 (1-237)  OY TACAAATATGAAAGCATTTTAAAGCAATTTGAATTGAAT	45 ArgasngluLeuPheLysSerMetGluGl 178 AGAATCGCTGAAGACTTGCAALACTATGG 179 AGAATCGCTGAAGACTTATGG 178 AGAATCGCTGAAGAGATACTATGGGAATACTATGGGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	295 GAAGGAGTCTTATACAAAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTAC 297  B5 HisGlyLysLeuTyrArgalaileLeuLeuAepValSerLysArgLeuLysAla 104  296 BACAAGAAAACTGAAACGACTTTAATTGAACAAACATGCTTTCTAAAATCTTGGAAGA 357  105 AspLysGluMetSerThrPheGluIleGluGlnGluLeuLeuGluGlnPheLeuArgAsn 124  Qy 358 AGTTTGGAAGAAATGGATGATGAA

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A;Residues: 1-206 <STO>
A;Cross-references: GB:AE005174; NID:g12512690; PIDN:AAG54312.1; GSPDB:GN00145; UMGP:?
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                           569 TGATTGCCCCCA---AGCGATAAACCACGCCCTAGAATGGTTTTTGCGACCGCATTCGCA 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 SerProAlaileSerCysGlnLeuArgArgCysCysSerGlyCysProSerIleAspLeu 162
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heat shock protein htgA - Escherichia coli (strain K-12)
NyAlternate names: heat shock protein Y
C;Species: Escherichia coli
C;Species: Bsep-1993 #sequence revision 18-Nov-1994 #text_change 31-Mar-2002
C;Accession: A40623; A56688; D64721; S28460
                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ProAlaProArgSerLysProCysProSerThrLeuIleAlaAlaTrpValArg
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                                                                                                                                                                                                                                                                                                                                     ACCCCTGTAATGATCCAGCCAACAGGACCTGTTAAAAAGCTCAGAGTTCTTGTAAGCACC
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C;Superfamily: Escherichia coli heat shock protein htgA
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A; Molecule type: DNA
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TCTTCATCATCC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 ATTICITCCAAACTICITICIAAGAITTTAGAAAGCAIGTTTTGTICAATTAAAGTGGT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGITITCTTGTTGTAATTGACCTTTAATTTATCGCACACACACGCATAAAATCTCTTTG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrasnLeuProCysProArgSerLeuLeuAlaIleLeuSerProProLysCysAsn 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AsnSerSerLeuArgIleSerThrLeuGluArgArgValLeuProPheSerLeuTrpVal 182
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-----ProAlaProArgSerLysProCysProSerThrLeulleAlaAlaTrpValArg 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 ACHAIGACAGCIAAIIGAIAAGAIIIIAAAA-----CCCCCCCAIIIIIAAACAGCGIIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGIALICIAIGGAGCIGGICAGILTITICALIGIGICITITITICGCCGICITIACCAAAA
                                                                                                                                                                                                                          629 ACGCCTGTAATGATCCAGCCAACAGGACCTGTTAAAAAGCTCAGAGTTCTTGTAAGCACC
                                                                                                                                                                                                                                                                                                569 TGATTGCCCGCA---AGCGATAAACCACGCCCTAGAATGGTTTTTGCGACCGCATTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                     SerSerSerPheThrLeuAlaSerThrAlaCysArgAsnSerCysLeuCysSerSer
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|I|ePhePhedinValLeuArgArgAsnCysSerSerAsnCysCysSerIleSerAsnVal
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                                                    206
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Conservative:
Mismatches:
Indels:
Escherichia coli heat shock protein
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 C; Superfamily:
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eorgopo 2613-2 2613-2 richia : A4062 ary ary cMIS>	Db 103 AsplleSerLeuSerAlaPheSerPheAsnArgPheGluThrSerSerLysMetAlaArg 122  Qy 251 TATAAGACTCCTTCGCCTTTAATGAAACTCGCAAAACTATTGCTCCCATAGTATTGCAAC 192
Ridames, R.; Dean, D.O.; Debbage, J. DNS seq. 3, 327-332, 1993 DNS seq. 3, 327-332, 1993 DNS seq. 3, 327-332, 1993 DNS seq. 3, 327-332, 1993 DNS seq. 3, 327-332, 1993 A;Reference number: A56683, MUID:94003405; PMID:8400364 A;Acession. A5668	RESULT 14 C89910 hypothetical protein SA1181 [imported] - Staphylococcus aureus (strain N315) C,Specials: Staphylococcus aurecus (strain N315) C,Specials: Staphylococcus aurecus in Havar-2001 #sequence revision 10-May-2001 #tequence revision 10-May-2001 #tequence revision 10-May-2001 #tequence revision 10-May-2001 #text change 22-Oct-2001
A;Molecule type: DNA A;Residues: 36-196 <jam> A;Cross-references: ZME:X67700; NID:g41754; PIDN:CAA47932.1; PID:g41757 R;Blattner, F.R; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co</jam>	C; Accession: C89910 R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1925-1940, 2001
Science 277, 1453-1462, 1997 Science 277, 1455-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: D644721	A;Title: Monle genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Recession: C89910 A;Status: preliminary A;Status: preliminary
DNA 6 <blat> 6 <blat> 6 SIATOCOLI12; GB:U00096; NID:g1786192; P curce: strain K-12, substrain MG1655 certain whether Met-1 (CTG) or Met-36 is th</blat></blat>	A;Residues: 1-1009 <kur> A;Residues: 1-1009 <kur> A;Cross.references: GB:BA000018; PID:g13701144; PIDN:BAB42439.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: SA1181</kur></kur>
V, Generally, htpV A, Map position: 0 min A, Start codon: CTC C, Superfamily: Bscherichia coli heat shock protein htgA C, Keywords: heat shock; stress-induced protein	ores: 2.56 98.50 larity: 37.88% imilarity: 22.53%
: 0.0295 Length: 122.00 Matches:	.0 (1-1009)
Percent Similarity: 34.41* Conservative: 12  Pest Local Similarity: 31.10\$ Mismatches: 65  Query Match: 2.05\$ Indels: 36  DB: 2 Gaps: 5	Oy 13 TATGATAGAGACTTGGAATTTTTAAAGCAATTGGAA 48
-09-732-091-3 (1-759) x A40623 (1-196)	49 TCTAGTGATTTATTGGATTTGTTTGAGGTGCTTGTTTTTGGTAAAGAGGGGGAAAAAGA 10
Oy 629 ACGCTGTAATGCAGCCAACAGGACCTGTTAAAAAGCTCAGAGTTCTTGTAAGCACC 570	Db 728 LeuThrAspAspAspAspIleAsnGluIleIleAlaTrpArgGlyGluGluGluGlu /46  Qy 109 CACAATGAAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAA 168
OY 569 TGATTGCCCGCAAGCGATAAACCACGCCCTAGAATGGTTTTTGCGACCGCATTCGCA 513	Db 747
Qy 512 ACAATGACAGCTAATTGATAAGATTTAAAACCCCCCATTTTAAACAGCGTTAAA 459	Db 757 ArgryrHisGluPheGluMetGluIleAlaArgLeuGluSerLeu 771 Oy 229 ATTAAAGGCGAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGTGGATAAATTAAAG 288
8 GTCGCCGCGCTTAAGGCTTGTCTGTTTAAATTGTCCGTGTTTTTTATGGATAATTCATCG 3 :::	2772
Qy 398 CACATTCTTTCACTTOTTCATCATCC 372	Db 785 AspGluTyrGluGlnLysLysGluLysMetAsnThrLeuIleAspGluTyrSerAlaVal 804  Qy 328
Qy 371 ATTICTTCCAAACTTCTTCTAAGATTTTAGAAGCATGTTTTGTTCAATTAAAGTCGTT 312	Db 805 HisTyrGlnCysGlnAsnAsnlleAsnLysThrGlnSerIleValSerHisIleAsnTyr 824  Qy 355 AGAAGTTTGGAAGAAATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATA 414
Qy 311 TCAGTTTTCTTGTTGAATTGACCTTTAATTTATCGCACCACGCATAAAATCTCTTTG 252	Db 825 LeuAsnGlnGluLeuLysAspGlnGluClePheGlnLeuAlaGluLleValSerGly 844

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31 LeuLeuAspLysGluLeuSerAspLeuArgAsnGlnAspGluGluMetThrArgGluArg 110
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ValLysGlnAlaValIleIleLysAlaSerValLysGluAsnAsnAsnValGluArgAsn 130
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131 Gluval------IleAsnLeuvalPheAlaGlyvalGlyPheValThrAlaGly 146
                                                                                                                                                                                                                                                                                                                                                                                                167 LeuLeulleLeuhisGlyAlaAsnAsnIleValGluSerGlyTyrTyrIleLeuTyrArg 186
         286 AAGGTCAATTACAACAAGAAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAA 345
                                                                                                                                                    GTGAAAGAA---ATGTGCGATGAATTATCCATAAAAAAACACGGACAATTTAAACAGACAA 441
                                                                                                                                                                                                                        442 GCCTTAAGCGGGGGGCTTTAACGCTGTTTAAAATGGGG---GGTTTTAAATCTTATCAA 498
                                                                                                                                                                                                                                                                                                                            147 LeuGlnIleValAlaGlyValGlyMetValGlySerValValGlySerlleProGlyThr 166
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                                            SerSerAspIleThrAlaLysValAsnThrGlyGluileThrThrGluThrAlaIleLys
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Job time: 27.5 secs
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AE0360
C;Paccession: AE0360
C;Paccession: AE0360
C;Paccession: AE0360
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C;Paccession: AE0360
I), M.; Rutherford, K.; Simmonds, M.; Scelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
Nature 413, 523-527, 2001
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92208.1; PID:g15980920; GSPDB:GN00175
C;Genetics:
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                                                                                                                                                                        ------IleArgArgGluAlaValSerHisGlyLeuSerGlyLeuGlu 896
                                                                                                                                                                                                                                                                                                                   -GlyGluThr 918
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----AGACAAGCC 444
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LysasnasniysasnieuThrieuGluasnPheValleuIleTyrTyrLeuaspGlnIle
                                                                  445 TTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGTTTTAAAATCTTATCAATTAGCT
                                                                                                                                        505 GTCATTGTTGCGAATGCGGTCGCAAAACCATTCTAGGGCGTGGTTTATCG-----
                                                                                                                                                                                                           ----CTTGCGGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTTAACA
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ALIGNMENTS

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-Q=(CGT2_1/USPFO spool/USO)9732091/runat_02072004_182406_19007/app_query.fasta_1.903
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-LOOPEXT=0 -UNITS=bits -GTART=1 -RND--1 -NATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOOTALIGN=200 -THR XCORE=pct -THR MINSO -ALIGN=15
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Copyright (c) 1993 - 2004 Compugen Ltd.
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STRAIN=26655 / ATCC 700392;
STRAIN=26655 / ATCC 700392;
STRAIN=26655 / ATCC 700392;
Toch U.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Kerchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Helicobacter pylori (Campylobacter pylori). Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter. The complete genome sequence of the gastric pathogen Helicobacter pylori.";
Nature 388:539-547(1997).
-!- SIMILARITY: Belongs to the UPP0174 family. 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein HP1588. NCBI\_TaxID=210; Venter J. HP1588 

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt\_42:\*

Database :

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID .	Description
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7	1270	94.1	253	Н	YF88 HELPJ	
m	637	47.2	209	Н	YF87 HELPY	O26106 helicobacte
4	630	46.7	209	Н	YF87 HELPJ	Q9zj25 helicobacte
Ŋ	265	19.6	237	,	YAAW ECOLI	P75617 escherichia
9	262	19.4	237	Н	YAAW_ECO57	P58316 escherichia
7	122	1,6	196	٦	HTGA_ECOLI	P28697 escherichia
60	105	7.8	726	٦	HS9A_BRARE	Q90474 brachydanio
9	16	7.2	916	7	SECA_TREPA	083394 treponema p
10	96.5	7.2	373	Н	BIOF_AQUAE	066875 aquifex aeo
ťί	95.5	7,7	344	Н	ABIC_LACLA	Q01457 lactococcus
12	95	7.0	517	Н	YC09_CAMJE	Q9pn86 campylobact
13	95	7.0	3214	rt	BPA1 HUMAN	Q03001 homo sapien
14	94.5	7.0	1433	Н	REST_CHICK	042184 gallus gall
15	93.5	6.9	802	Н	PAC BACME	Q60136 bacillus me
16	92.5	6.9	802	~	PAC_ARTVI	P31956 arthrobacte
17	92.5	6.9	892	М	RCQ1 CAESL	P46064 caenorhabdi
1.8	91.5	9.9	399	Н	RPSD_THEMA	P77994 thermotoga

EMBL; AE000656; AAD08627.1; -. PIR; D64718; D64718. TIGR; HP1588; -.

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                                                                                                                                                                                                           "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- SIMILARITY: Belongs to the UPF0174 family.
                                        Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                    MEDLINE=99120557; PubMed=9923682; King B.L., Brown E.D., Doig P Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis Crist T.J.;
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Matches:
Conservative:
Mismatches:
Indels:
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PIR; B71800; B71800.
InterPro; IPR05257; UPF0174.
Pfam; PF03567; UPF0174.
Hypothetical procein; Complete proteome.
SEQUENCE 253 AA; 28475 MW; 127158B2B1A2036A
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Best Local Similarity:
                                                                                   NCBI_TaxID=85963;
              Hypothetical
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 InterPro; IPR005367; UPF0174.
Pfam: PF03667; UPF0174, 1.
Hypothetical protein; Complete protecme.
SECURNCE 253 AA; 28417 MW; 00EI5A38B1A2036A CRC64;
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(Rel. 40, Last Bequence update)
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                                                                                  7.56e-96
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Best Local Similarity
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ALD YF88 HELPJ
DT 16-OCT-2001 (
DT 16-OCT-2001 (
                                                                       Alignment Scores:
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                GGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAACCATTCTA
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STRAIN=26695 / ATCC 700392;

STRAIN=269394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Relson K., Qackerbusk J., Zhou L., Kirkness B.F., Peterson S.,

Nocktons K., PitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Jiterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin B.,

Hayes W.S., Borodovsky M., Kaip P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished observations (OCT-2001).
-!- SIMILARITY: Belongs to the UPF0174 family.
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshift in position 160.
                                                                                                                                                                                                                                                                                                                GCCAATGGAGATAAGAAGTCGTTGCAAATAGAATCCATT 759
                                                                                                                                                                                                                                                                                                                                  AlaAsnGluAspLysLysSerLeuGlnIleGluSerVal 253
                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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Helicobacteraceae, Helicobacter.
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Nature 388:539-547(1997)
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
    proteome.
F98D3FB8F3F62323 CRC64;
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Conservative:
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11 protein; Complete
209 AA; 23069 MW;
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(Rel. 40, Last seq
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60.29%
47.22%
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  Hypothetical
SEQUENCE 20
                                                                      Alignment Scores:
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.;
                                                                                                                                                                                                                                                  Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                         coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
-!- SIMILARITY: Belongs to the UPF0174 family.
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77
44
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36
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=94003405; PubMed=8400354;
James R., Dean D.O., Debbage J.;
Five open reading frames upstream of the dnaK gene
DNA Seq. 3:327-332(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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A36682B2BA116747
                                                                                                                         YAAW ECOLI STANDARD; PRT; 237 AA. 197561; 047290; Created) 16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last senotation update) 16-CCT-2001 (Rel. 40, Last annotation update) 14ypothetical protein yaaw.
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EMBL; AE000112; AAC73122.1; -.
EIR; C64721; C64721.
ECGGene; EG14340; yaaW.
InterPro; IPR005367; UPF0174.
Ffam; PR03667; UPF0174; 1.
HYpochbetical protein; Complete proteome.
COMFLICT 190 190
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                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Escherichia.
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ArgAspGluGlyValLeuTyrLysGluIleLeuCysAspAlaCysAspHisLeuAspIle
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   Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Xills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                               two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                 proteome.
C6EC950CDD424CAF CRC64;
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122
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Matches:
Conservative:
Mismatches:
                                                                             "Genomic sequence comparison of two unrelated :gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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Pfam; PF03667; UPF0174; 1.
Hypothetical protein; Complete SEQUENCE 209 AA; 22907 MW;
                                                                                                                                                                                                                                                                                  EMBL; AE001571; AAD07072.1; -. PIR; A71800; A71800.
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630.00
75.49%
59.80%
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Best Local Similarity:
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                                                                                                          Hisdly LysLeuTyr ArgAlaile Leu Leu AspValSer Lys Arg Leu Lys Leu Lys Ala 104
                                                                                                                                              ThrTrpLysLysMetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg 144
                                                                                                                                                                                                                       GTGAAAGAAATGTGCGATGAATTATCCATAAAAAACAGGACAATTTAAACAGAAAGCC 444
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                    64
               ArgasnGluLeuPheLysSerMetGluGlyHisProGluGlnHisArgArgAsnTrpGln
                                                         leulleAlaGlyGluLeuGlnHisPheGlyGlyAspSerIleAlaAsnLysLeuArgGly
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                                            178 AGAATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGC
                                                                                                                                AACAAGAAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAAATCTTAGAAAGA
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STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935, PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Agodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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LeuGlnIleAlaCysLeuArg 229
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STRAIN=C157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                             AGTITGGAAGAAATGGATGATGAA
127 AGCTCCATAGAATACAAAAGG---
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YAAW OR ZOULI OR ECSO012.
Escherichia coli 0157:H7.
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ThrTrpLysLysMetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg 144
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACAAATATGATAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTGGAT
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ArgasnGluLeuPheLysSerMetGluGlyHisProGluGlnHisArgArgAsnTrpGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AGAATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGC
                                                                                                        comparison with a laboratory strain K-12.";
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44.5
90
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Matches:
Conservative:
                                                                                                                                                        DNA Res. 8:11-22(2001).
-!- SIMILARITY: Belongs to the UPF0174 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein; Complete 237 AA; 26681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE005178; AAG54311.1; -. EMBL; AP002550; BAB33434.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UPF0174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005367; UPF01
Pfam; PF03667; UPF0174; 1.
Hypothetical protein; Comp.
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48.99%
30.77%
19.42%
                                                                                                                                O157:H7 and genomic com
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; C85481; C85481.
PIR; C90630; C90630.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445
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505 GTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTAGGGCGTGGTTTATCGCTTGCGGGC 564

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US-09-732-091-3 (1-759) x HTGA ECOLI (1-196)
                                                                                                                                                                                                                                                  POLY-SER
                                                                                                                                              EMBL; X67700; CAA47932.1; ALT INIT.
                                                                                                                                                             EMBL; E03720; AAA23992.1; ---
EMBL; E03720; AAA2393.1; ALT INIT.
EMBL; AD10483; -; NOT ANNOTATED_CDS.
EMBL; AE000112; AAC73123.1; ---
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   be deleted in future releases.
                                                                                                                                                                                                                                 protein; Heat shock
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122.00
38.41%
31.10%
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                                                                                                                                                                                                                  PIR; A40623; A40623.
Hypothetical proteir
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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ID HS9A_BRARE

AC Q90474;

DT 15-JUL-1999

DT 16-OCT-2001
                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                     684
                                                                                                                      GlyValLysAla-----ValSerGlySerSerTyrArgValThrIleProAlaVal 222
624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "THE COMPLETE GENOME SEQUENCE OF ESCHETICHIA COLI K-12.";
Science 277:1453-1474(1997).

-! FUNCTION: NOT KNOWN, REQUIRED FOR HIGH-TEMPERATURE GROWTH OF

E. COLI. IT IS POSSIBLE THAT HYGA PROTEIN SOMEHOW REGULATES BITHER

TRANSCRIPTION OF THE RPOH GENE OR THE ACTIVITY OF ITS GENE PRODUCT

SIGMA-32. PLAYS A ROLE OPPOSITE THAT OF DMAK, DNA, AND GRPE IN

TERMS OF HEAT SHOCK REGULATION, ANTAGONIZING THE NEGATIVE OF

THESS AND THUS FINE-TUNING THE HEAT SHOCK RESPONSE.

-! ORUTION: By high temperatures.

-! CAUTION: It is uncertain whether Met-1 or Met-36 is the initiator.

-! CAUTION: Ref.3 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frameshift. CAUTION: This sequence, according to the EcoSeq database (K. Rudd) is probably not a real protein; therefore this entry will probably
                                             AATCAGGTGCTTACAAGAACTCTGAGCTTTTTAACAGGTCCTGTTGGCTGGATCATTACA
                                                                        -- AlaglyúeuglyélyérovalólyalaAlaLeuAsn
                                                                                                   GGCGTATGGACAGCGATTGATATTGCAGGGCCGGCTTATAGGGGTAACCATACCGGCATGC
                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Wery hypothetical heat shock protein htgA (Heat shock protein htpY)
HTGA OR HTPY OR B0012.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    James R., Dean D.O., Debbage J.; "Five open reading frames upstream of the dnaK gene of B. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yura I., Mori H., Nagai H., Nagata I., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; "Systematic sequencing of the Escherichia coli genome: analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEATH=K12 / W3110;
MEDLINE=93239687; PubMed=8478327;
Missiadras D., Georgopoulos C., Raina S.;
"The Escherichia coli heat shock gene htpy: mutational
cloning, sequencing, and transcriptional regulation.";
J. Bacteriol. 175:2613-2624(1993).
                                                                                                                                                                                                                                                196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992)
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                              685 ATTGTGGTTGCCACTTTACGC 705
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=94003405; Pubmed=8400364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                STANDARD:
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STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on itse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@aibe.sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629 ACGCCTGTAATGATCCAGCCAACAGGACCTGTTAAAAAGCTCAGAGTTCTTGTAAGCACC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 ACAATGACAGCTAATTGATAAGATTTAAAA-----CCCCCCCATTTAAACAGCGTTAAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 GTCGCCGCGCTTAAGGCTTGTCTGTTTAAATTGTCCGTGTTTTTTTATGGATAATTCATCG 399
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17 -----ProAlaProArgSerLysProCysProSerThrieuIleAlaAlaTrpValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569 IGATIGCCCCCA---AGCGAIAAACCACGCCCIAGAAIGGIITITIGCGACCGCAITCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 LysMetArgValSerTrpLeuGluSerLysCysAspThrProPheAlaAsnAsn----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TCTTCATCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 ATTTCTTCCAAACTTCTTTCTAAGATTTTAGAAAGCATGTTTTGTTCAATTAAAGTCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 AA; 21225 MW; ECA6154160A40993 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
51
12
12
65
36
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
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(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ž
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-----AsnLeuValSer---ValThrLysGluGlyLeu 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 TATAGGGTAACCATACCGGCATGCATTGTGGTTGCCACTTTACGCCTAAAAACACGCAA 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: ;:: 575 LyslyslleGluLysValThrValSerAsnArgLeuValSerSerProCysCysIleVal 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ATTGATATTGCAGGCCGGCT 660
                                                                                        247 TTATACAAA----GAGATTTTATGCGATGTGTGCGATAAATTTAAAGGTCAATTACAACAAG 303
                                                                                                                                                                                                                                                                                                                                       364 GAAGAAATGGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAACACG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAATTTAAACAGACAAGCCFTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IleMetLysAspileLeuAsp 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 CGIGGIFIATCG-----CTIGCGGCCAAICAGGIGCITACAAGAACICIGAGCITITIA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                595 ThrserThrTyrdlyTrpThrAlaAsnMetGluArgIleMetLysSerGlnAlaLeuArg 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spirochete.";
Science 281:375-388(1998).
Science 281:375-388(1998).
-!- FUNCTION: Involved in protein export. Interacts with the secY/secE subunits. SecA has a central role in coupling the hydrolysis of ATP to the transfer of pre-secretory periplasmic and outer membrane proteins across the membrane (By similarity).
                                                                                                                                             513 IleTyrMet11eGluPro11eAspGluTyrCysValGlnGlnLeuLysGluTyrAspGly
                                                                                                                                                                                                                                                                                                                                                                                                544 GluLeuProGluAspGluGluGluLysLysLysGluAspGluLeuLysAlaLys---Tyr
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      |\cdot|\cdot| LysAspGInValAlaAsnSerAlaPheValGIuArGLeuArGLysAlaGLyLeuGIuVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Complete genome sequence of Treponema pallidum, the syphilis
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Last annotation update)
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STRAIN-Nichols;
MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721 GCCAATGGAGATAAG 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 GluAsnLeuCysLys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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LeuSerAspLeuLeuArgTyrTyrThrSerAlaSerGlyAspGluMetValSerLeuLys 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGGATITIGITIGAGGIGCITGITITIGGIAAAGACGCGAAAAAAAGACACAAIGAAAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuAspLeuPheThrGluLeuAlaGluAspLysAspAsnTyrIysLysTyrTyrGluGln 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FheSerLysAsnileLysLeuGlylleHisGluAsp-----SerGlnAsnArgLysLys 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 AspTyrValSerArgMetLysAspThrGlnLysHisIleTyrTyrileThrGlyGluThr 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GGAGTC 246
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                                               Bractydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         zebrafish and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the heat shock protein 90 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>B</u>
                                                                                                                                                                                                                                                                        Lele Z., Hadfi S., Sass J.B., Krone P.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          SECUENCE OF 36-136 FROM N.A.
MEDILINE=95071389; PubMed=7980538;
Krone P.H., Sass JB.
"HSP 90 alpha and HSP 90 beta genes are present in the are differentially regulated in developing embryos.";
Biochem. Biophys. Res. Commun. 204.746-752(1994).
-!- FUNCTION: Molecular chaperone. Has ATPase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Heat shock.
726 AA; 83561 MW; F7DEB8EF1FBC9CEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726
61
41
75
108
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Mismatches:
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Matches:
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InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR001404; Hsp9d.
Pfam; PF0018; HATPase c; 1.
Pfam; PF00183; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-732-091-3 (1-759) x HS9A_BRARE
protein HSP 90-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF068773; AAC21567.1; -.
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SWART; SM00387; HATPASE C; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L35586; AAA97518.1; -. PIR; JC2343; JC2343.
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105.00
35.79%
21.40%
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                             NCBI_TaxID=7955;
                               HSP90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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   shock
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                                                                                                    ---AlaLeuLeuArgThrArgGlyValLy6HisGluValLeu 486
                                                                                                                                                                                         487 AsnAlaLysAsnHisAlaArgGluAlaLeuileIleAlaGluAlaGlyAlaLysGlySer 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 392:353-358(1998).

-!- CATALYTIC ACTIVITY: 6-carboxyhexanoyl-CoA + L-alanine = 8-amino-7-oxononanomate + CoA + CO(2).

-!- COFACTOR: Pyridoxal phosphate (By similarity).

-!- COFACTOR: Pyridoxal phosphate; first step.

-!- PATHWAY: Biotin biosynthesis; first step.

-!- SIMILARITY: Belongs to class-II of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                     456 GlyGlnProvalLeuValGlyThrIleSerIleGluLysSerGluLysLeuSer-----
                                                                                                                                                                                                                                                                                                                                                                                                             30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
8-amino-7-oxononanoate synthase (EC 2.3.1.47) (AONS) (8-amino-7-ketopelargonate synthase) (7-keto-8-amino-pelargonic acid synthetase)
(7-KAP synthetase) (L-alanine--pimelyl CoA ligase).
                                                                442 GCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGTTTTAAATCTTATCAATTA
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                                                                                                                                                                                                                                        ----TIATCGCTTGCGGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=99196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Deckert G., Marren P.V., Gasterland T., Young W.G., Lenox A.L.,
Schahm D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber J.
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                   -----GCTGTCATTGTTGCGAATGCG--
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Matches:
                                                                                                                                                                                                                                          -----GICGCAAAACCATICIAGGGCGIGGI-
                                                                                                                                                                                                                                                                                                                                                                     373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASS 2; 1.
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InterPro; 1PR003408; Ala synthase.
InterPro; 1PR004839; Aminotrans_I/II.
InterPro; 1PR001917; Aminotrans_II.
InterPro; 1PR004723; BioF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02490; ALA Bynchase; I. Pfam; PF00155; aminotran 1 2; I. TIGREAMS; TIGR00858; bioF; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42532 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOF OR AQ 626.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
Score:
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066875;
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: :::||| :::||| :::||| :::
380 AlaThIIeThrPheGlnAsnPhePheArg-------MetTyILy8Ly8LeuSer 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: :::||||||
LeuSerGluGluGluTrpSerAlaIleCysAspGluIleLysGluAlaHisThrArg 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 PheLysTyr-----IleHisTyrPheThrGlnAlaLeuArgAlaHisLeuLeuTyr 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 ArgalaaspvalaspTyrValValLysaspGlyGlnValGlnIleValAspGluPheThr 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 GlyMetThrGlyThrAlaAspThrGluAlaLeuGluLeuAsnLysIleTyrLysLeuGlu 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGACTITAATIGAACAAACAIG---CITICIAAAAICITAGAAAGAAGTITGGAAGAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValValValLeuProThrAshLeuProValAlaArgValAspGluHisAspValValTyr 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TTATCCATAAAAACACGGACAATTTAAACAGACAA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 GlyArglleLeuGluGlyArgArgTyrSerAspGlyLeuHisGlnAlalleGluAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 AGGCATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 GGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAGATT---
        SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secA, secB, secD, secE, secF, secG and secY (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS, PRO0006; SECA.
PRINTS, TICRO0065; SECA; 1.
PROSITE; PS01312; SECA; 1.
Protein transport; ATP-binding; Membrane; Translocation; Transport;
                                                       similarity).
SUBCELLULAR LOCATION: Cytoplasmic side of plasma membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EASS61FGEE7C65AE CRC64
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL)

    -!- SIMILARITY: Belongs to the secA family.

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                                                                                                                                                                                                                                                                       entities requires a license agreement (St or send an email to license@isb-sib.ch).
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TIGR; TP0339; -
Interbro; IPR004027; SEC C_motif.
Interpro; IPR000185; SecA.
Pfam; PF02810; SEC-C; 1.
Pfam; PF01043; SecA_protein; 1.
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97.00
40.17%
21.76%
7.19%
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MP BIND 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 AspLeufysArgLeuThrGlnIleCysGluGluTyrAspCysMetLeuTyrIleAspGlu 192
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SerLeullePheSerThr---SerLeuProProSerValCysAlaGlyAlaLysAla 266
                                                                                                                                 TTTGGTAAAGACGGGGAAAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAA 144
                                                                                                                                                                                                                                                                          -----GAAGGAGTCTTATAC 252
                                                                                                                                                                                                                                                                                                                        253 AAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAACAAGAAAACTGAA 312
                                                                                                                                                                                                                                                                                                                                                                       GATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAACACGGACAATTTA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| |||||||::::::|||
|139 AspTyrGluGluLeuGluGluPheLeuLys------LysAsnArglysPhe 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgargvalLeulle-----IleThrAspThrValPheSerMetAspGlyAspValAla 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TITIAAAICITAICAAITAGCIGICAITGITGCGAAT 519
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                                                                                                                                                                                               52 LysGluAlaGlyLeuGlySerGlyAlaSerGlnLeuValSerGlyTyrThrLysHisHis 71
                                                                                                                                                                                                                                          ::: |||:::||| :::::: |||::: ||| 72 ArgGluLeuGluGluLeuPheGly 91
                                                                                  TIGGAAITITIAAAGCAAITGGAAICTAGIGAITTAITGGAITITGAGGIGCTIGIT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 ACAGGCGTATGGACAGCGATTGATATTGCAGGGCCGGCTTATAGGGTAACCATACCGGCA
                                                                                                                                                      -GiyLeuArgLysHisProGluValValGluGluSerileArgValLeu
                                                                                                                                                                              ----GATGATTACGCTAAATACGCA
                                                                                                                                                                                                                             -CAATACTATGGGAGCAATAGTTTTGCGAGTTTCATT
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                                                                                                                                                                                                                                                                                                  92 SerdiyPheLeuAlaAsnValGlyThrIleProAlaLeuValGluGluGlyAspLeu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGTCGCAAAACCATTCTAGGGCGT---GGTTTATCGCTTGCGGGCAATCAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 AACAGACAAGCCTTAAGCGCGGGGGCTTTAACGCTGTTTAAATGGGGGGT
                                                                                                                                                                                                                                                                                                                                                 --GluLeuAsnHis----
  40
102
77
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|LeuGluGlyValLysAspPheCysSerAspAspTyrLeu-
Conservative:
Mismatches:
Indels:
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(Rel. 27, Last sequence update)
                                                           (1-373)
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                                                             AQUAE
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                                                                                                                                                                                                                                                                                                                                                  -----ValLeuSerAsp-
 36.75%
22.61%
7.15%
                                                             x BIOF
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IleGluIle 269
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                                                             US-09-732-091-3 (1-759)
                                                                                                                                                                                                                                                                              232 AAAGGC---
  Percent Similarity:
Best Local Similarity:
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ABIC_LACLA
ID ABIC_LACLA
AC 001457;
DT 0.-0CT-1993 (
DT 01-0CT-1993 (
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GlnLysValGluLeuVallleSerArgGln 197
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                                                                                              plasmid pIN20.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                         resistance
                                                                                                                                                                                                                                                                          Durmaz B., Higgins D.L., Klaenhammer T.R.;
"Molecular characterization of a second abortive phage resistan
gene present in Lactococcus lactis subsp. lactis ME2.";
J. Bacteriol. 174:7463-7469(1992)
-:- FUNCTION: PROVIDES RESISTANCE TO BACTERIOPHAGE BY ABORTIVE
                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
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Mismatches:
Indels:
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01-OCT-1993 (Rel. 27, Last annotation update)
Abortive phage resistance protein abiC.
ABIC OR PRF.
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Matches:
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95.50
40.95%
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|GluGluAsnSerArgGluGlnIleAlaHisIleValArgLysTyrGluGluGluAlaLys 180
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                                                                  4 GCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTG
                                                                                                                                64 GATTTGTTTGAGGGCCTTGTTTTTGGTAAAGACGGCGAAAAAAGACACAATGAAAAACTG
                                                                                                                                                              ----LysLysLysTyrGluGluLysThr
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(Dystonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  GATGTGTGCGATAAATTAAAGGTCAATTACAACAAGAAAACTGAAACGACTTTA-
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Q03001; Q12825; Q13266; Q13267; Q13775; Q96076; Q90GD7;
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22-SFRB-2003 (Rel. 41, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Bullous pemphigoid antigen 1 isoforms 1/2/3/4/5/8 (230 kDa. pemphigoid antigen 1 isoforms protein)
Pemphigoid antigen (BPA) (Hemidesmosomal plaque protein) (BPAGI OR DWH OR TOR KIAA0728.
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                                 US-09-732-091-3 (1-759) x YC09_CAMJE (1-517)
                                                                                                                                                                62 AlaGluLeuĠluval---
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                                 245
                                                                  543
                                                                                             ---SerGluGluLeuValVallleLeulleAsnSerLeuTyrValLysArgGlyLeuGly 264
 486
 AATTTAAACAGACAAGCCTTAAAGCGCGGCGACTTTAAACGCTGTTTAAAAATGGGGGGTTTT
                                                                  487 AAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTC---GCAAAAACCATTCTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-20150912; PubMed=10688204; Parkhill J. Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Quail M.A., Railyshev A.W., Moule S., Pallen M.J., Penn C.W., Whitehead S., Barrell B.G.; Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; Treveals hypervariable sequences of the food-borne pathogen Campylobacter jejuni Nature 403:665-668 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA-binding; Complete proteome.
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Campylobacteraceae, Campylobacter.
NGBI_TaxID=197;
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Mismatches:
Indels:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last arnotation update)
Hypothetical UPF0144 protein Cj1209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the UPF0144 family.
-!- SIMILARITY: Contains 1 HD domain.
-!- SIMILARITY: Contains 1 KH domain.
                                                                                                                                                                                                                                   517 AA
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Matches:
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InterPro: IPR003607; MeT_phsphohydro.
InterPro: IPR003675; Unchar_HDIG.
Pfam; PP01966; HD; 1.
Pfam; PP00013; KH; 1.
SMART; SM004014; HDC; 1.
SMART; SM00322; KH; 1.
TIGRPAMS; TIGR00277; HDIG; 1.
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                                  238 GlyIleLeuArgThrGlnLeuSer---
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HAMAP; MF_00335; -; 1.
InterPro; IPR006674; HD.
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STRAIN-NCTC 11168;
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Best Local Similarity:
Query Match:
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Stanley J.R., Tanaka T., Mueller S., Klaus-Kovtun V., Roop D.; "Isolation of complementary DNA for bullous pemphigoid antigen by use of patients' autoantibodies."; J. Clin. Invest. 82:1864-1870(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparison of molecularly cloned bullous pemphigoid antigen to desmoplakin I confirms that they define a new family of cell adhesion
                                                                                                                                        Elgart G.M., Stanley J.R.; "Cloning of the 5' mNA for the 230-kD bullous pemphigoid antigen by rapid amplification 101CNA ends."; "Invest. Dermaton 101CNA ends.";
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MEDLINE=96199235; PubMed=8621649;
Tang H.-Y., Chaffotte A.-F., Thacher S.M.;
"Structural analysis of the predicted coiled-coil rod domain of the cytoplasmic bullous pemphigoid antigen (BPAG1). Empirical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=94280413, PubMed=8010969,
Hopkinson S.B., Jones J.C.,
"Identification of a second protein product of the gene encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 2160-2767 FROM N.A.
MEDIINE=91216368; PubMed=2090522;
Owaribe K., Kartenbeck J., Stumpp S., Magin T.M., Krieg T.,
Diaz I.A., Franke W.W.;
"The hemidesmoscral plaque. I. Characterization of a major
constituent protein as a differentiation marker for certain forms
            TISSUE=Keratinocytes;
MEDLINE=22011493; PubMed=1717441;
Sawamura D., Li K., Chu M.-L., Uitto J.;
Human bullous pemphigoid antigen (EPAG). Amino acid sequences deduced from cloned on the predict biologically important peptide segments and protein domains.";
                                                                                                                                                                                                           TISSUE=Fetal brain, and Retina;
MEDLINE=96121334; PubMed=8575775;
Brown A., Dalpe G., Mathieu M., Kothary R.;
"Cloning and characterization of the neural isoforms of human
                                                                                                                                                                                                                                                                                                             Laird G.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  Geerts D., Sonnenberg A.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Keratinocytes;
MEDLINE=91286285; PubMed=1712022;
Tanaka T., Parry D.A.D., Klaus-Kovtun V., Steinert P.M. Stanley J.K.
                                                                                                                                                                                                                                                                                              SEQUENCE OF 321-3214 FROM N.A. (ISOFORMS 1 AND 4).
                                                                                                                                                                                                 5
                                                                                                                                                                                                 SEQUENCE OF 1-645 FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1082-3214 FROM N.A. (ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 2287-3214 FROM N.A. (ISCFORM 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 2462-3214 FROM N.A. (ISOFORM 8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unction plaque proteins.";
7. Biol. Chem. 266:12555-12559(1991)
                                                                              Biol. Chem. 266:17784-17790(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89067122; PubMed=2461961;
                                                                                                                              PubMed=8345227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epithelia.";
Differentiation 45:207-220(1990).
  SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                      SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human epidermal autoantigen.";
Biochem. J. 300:851-857(1994).
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 392-492 FROM N.A.
TISSUE-Pineal gland;
                                                                                                                                                                                                                                                                      Genomics 29:777-780 (1995)
                                                                                                                    TISSUE=Keratinocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Keratinocytes;
                                                                                                                              MEDLINE=93346806;
                                                                                                                                                                                                                                                            dystonin
                                                                                                                                                                                                                                                                                                         Laird
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                                                                                                                                                                                                                                                                                              actin cross-linking factor).";
J. Biol. Chem. 277:6682-6687(2002).
-! FUNCTION: Cytoskeletal linker protein. Anchors keratin-containing
-! FUNCTION: Cytoskeletal linker protein. Anchors keratin-containing
-! intermediate filaments to the inner plague of hemidesmosomes. The
proteins may self-aggregate to form filaments or a two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease.
                                                                                                                                                                                        Okumura M., Yamakawa H., Ohara O., Owaribe K., "Novel alternative splicings of BPAGI (bullous pemphigoid antigen 1) including the domain structure closely related to MACF (microtubule
                                                                                            TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSP_005056, VSP_005057, VSP_005060,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=094833-1; Sequence=External;
Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Highly expressed in skeletal muscle and
globular domain-rod boundary.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DISEASE: BPAG1 is an autoantigen of bullous pemphigoid [MIM:600088], an autoantigen eubepithelial skin blistering el-struckarry: Belongs to the plakin or cytolinker family.
-!- SIMILARITY: Contains 1 actin-binding domain.
-!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 plectin repeats.
-!- SIMILARITY: Contains 4 spectrin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comment=Isoforms 1, 2, 5 and 8 are or may be fragments;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=003001-6; Sequence=VSP_C05062, VSP_005063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=4;
IsoId=Q03001-4; Sequence=VSP_005054, VSP_005056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2;
IsoId=Q03001-2; Sequence=VSP_005053, VSP_005055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSP_005065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isola=vo-v--
Name=3; Synonyms=le;
Isold=Q03001-3; Sequence=VSP_05558,
VSP_05558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP 005064,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1;
IsoId=Q03001-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                me=6; Synonyms=EA;
IsoId=094833-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=7; Synonyms=EB;
IsoId=Q8WXK8-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=C94833-3; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Homodimer.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U31850; AAC50243.1; -.
U31851; AAC50244.1; -.
AL096710; -; NOT ANNOTHED_CDS.
AY032900; AAX63130.1; -.
                                                                                                                                 TISSUE=Keratinocytes;
MEDLINE=21839111; PubMed=11751855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M69225; -; NOT ANNOTATED_CDS
EMBL; L11690; AAA52288.1; -.
localization of the N-terminal glo
J. Biol. Chem. 271:9716-9722(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY032901; AAK63131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M63618; AAA35606.1; -. X58677; CAA41528.1; -. M22942; AAA35538.1; -. U04850; AAA57184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cultured keratinocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q03001-5;
                                                                                                   SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=10;
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BMBL;
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EMBL;
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                                     2212 LysCysLeuGluGluAspLeuAlaLysSerGlnAsnLeuValSerGluPheLysGlnLys 2231
                                                                                                                                                                                        |||||||::: :::|||
2232 CysAspGlnGlnAsnIleIleIleGlnAsnThrIysLysGluValArgAsnLeuAsnAla 2251
                                                                                                                                                               ---- AAAAACACGACAATTTAAACAGA 438
               ---AATTACAACAAGAAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAAATC 348
                                                                                        GAAGAAGTGAAAGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griparic L., Keller T.C. III, "Identification and expression of two novel CLIP-170/Restin isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed predominantly in muscle.";
Biochim. Biophys. Acta 1405:35-46(1998).
-!- FUNCTION: SERNS TO BE A INTERNEDIATE FILAMENT ASSOCIATED PROTEIT THAT LINKS EMDOCYTIC VESICLES TO MICROTUBULES (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE CYTOSKELETON (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98137792; PubMed-9469933;
Griparic L., Volosky J.M., Keller T.C. III;
"Cloning and expression of chicken CLIP-170 and restin isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=042184-2; Sequence=VSP_000761;
Name=3; Synonyms=CLIP-170(11);
Isold=042184-3; Sequence=VSP_000762, VSP_000763;
Name=4; Synonyms=CLIP-170(11+35);
Isold=042184-4; Sequence=VSP_000764;
SIMILARITY: Contains 2 CAP-Gly_domains.
                                                                                                                                                                                                                                                                                                               RESULT 14

REST CHICK

AC 042184; 04228; 057563; 057564;

DT 15-UUL-1998 (Rel. 36, Last sequence update)

DT 10-UT-2003 (Rel. 42, Last annotation update)

DF REST (Rel. 42, Last annotation update)

DE Restin (Cytoplasmic linker protein-170) (CLIP-170).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bvent=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 17-1139 FROM N.A. (ISOFORMS 3 AND 4)
                                                                                      --TTAGAAAGAAGTTTGGAAGAAATGGATGAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=1;
IsoId=042184-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to licensegisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pectoralis muscle;
MEDLINE=99002898; PubMed=9784600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF014012; AAC60344.1; -.
EMBL; AF020764; AAC60345.1; -.
EMBL; AF045650; AAC03547.1; -.
                                                                                                                                                                 TGCGATGAATTATCCATA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 206:195-208(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           2252 Glu 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                            439 CAA 441
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                   292
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2175 ArgCysGluhlaLeuLysIleGlnAlaAspGlyPheLysAspGlnLeuArgSerThrAsn 2194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeulysGluGlnPheGluLysSerHisGluGlnLeuLeuGlnAsnIleLysAlaGluLys 2114
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                                                                                        GO; GO:0005604; C:basement membrane; TAS.
GO; GO:0005737; C:cytoplasm; IEP.
GO; GO:0005730; C:cytoplasm; IEP.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEP.
GO; GO:0007010; P:cytoskeleton organization and biogenesis; TAS.
GO; GO:0045104; P:intermediate filament cytoskeleton organiza. .; IEP.
InterPro; IPR001589; Actbind actnin.
InterPro; IPR001104; Plectin_repeat.
InterPro; IPR001525; SH3.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2135 GluMetLeuLysGlnLysValGluGluLeuThrArgGlnAsnAsnGluThrLysLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2155 MetGlrArgileGinAlaGluSerGluAsnIleValLeuGluLysGlnThrIleGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATACAAATATGATAGAGACTTGGAATTTTTAAAG-----CAATTGGAATCTAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GAGGTGCTTGTTTTGGTAAAGACGGCGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 AGACACAATGAAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2115 GluAsrAsnAspLysileGlnArgLeuAsnGluGluLeuGluLysSerAsnGluCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 AAATACGCAGAAAGAATCGCTGAAGAGTTG-----CAATACTATGGGAGCAATAGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; Actin-binding; Coiled coil; Repeat; SH3 domain;
Structural protein; Cytoskeleton; Cell adhesion; Calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLOBULAR 1.
CENTRAL FIBROUS ROD DOMAIN.
GLOBULAR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3214
46
35
35
62
38
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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CH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-732-091-3 (1-759) x BPA1_HUMAN (1-3214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                        SMART; SM00033, CH; 2.
SMART; SM0150; SPEC; 2.
PROSITE; PS50002; SH3; FALSE_NEG.
PROSITE; PS00019; ACTININ 1; 1.
PROSITE; PS00020; ACTININ 2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 GTGTGCGATAAATTAAAGGTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calcium-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                   Pfam, PF00681, Plectin, 5.
Pfam, PF00018; SH3, 1.
Pfam, PF00435; spectrin; 3.
                                                                                                                                                                                                                                                                                 Pfam; PF00307; CH; 2.
Pfam; PF00681; Plectin; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.75%
25.41%
7.04%
   AAA57185.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.61
EMBL, U04850; AAA57185.1;
PTR; 156317; A40937.
Genew; HGNC:1090; BPAG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä; 5
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851
959
1077
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3214
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322
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1670
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DOMAIN
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DB:
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SPACER PEPTIDE
517 AATGCGGTCGCAAAACCATTCTAGGGCGTGGT-
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STRAIN=ATCC 14945;
MEDLINE=95180705; PubMed=7875576;
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EMBL; Z37542; CAA85774.1; -...
EMBL; AF161313; AAD45609.1; -...
PIR; S49252; S49252.
HSSP; P06875; LAJQ.
MEROPS; S45.001; -...
                                                                                                                                                   STANDARD;
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234
265
                                                                                                                                                                                                                                                                              Bacillus megaterium.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=ATCC 14945;
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                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1404;
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25
235
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                                                                                                         coil; Repeat; Alternative splicing.
                                                                                                                                                                                                                                       TOTKLEHARIKELEGSLLFEKTKADKLQRELEDTR
RQISEDPEN (in isoform 3).
/FIId=VSP 000762.
S -> GGSSKVS (in isoform 3)
                                                                                                                                                                                                                                                    -> R (IN REF. 2; AAC03547).
-> V (IN REF. 2; AAC03548).
5631CB8683498E23 CRC64;
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52
36
74
51
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COILED COIL (POTENTIAL)
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Mismatches:
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Matches:
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CAP-GLY 2.
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                                                                                                                            CAP-GLY
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                                                                                                            Coiled
              InterPro; IPRO:1918; CAP-G1y.
InterPro; IPRO:1918; InterPro; PRO:1918; CAP-G1y.
Pfan, PF0.1302; CAP-G1X; Z.
SMART; SM00343; ZNF C2HC; 1.
PROSITE; PS00845; CAP-G1X 1. 2.
PROSITE; PS0245; CAP-G1X 2; Z.
Cytoskeleton; Microtubule; Colled
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24.41%
7.01%
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Best Local Similarity:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 1170 AsnvallysLeuAlaGluGluLeuGlyArgSerArgAspGluValThrSerHisGlnLys 1189
549
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Pfam; PF01804; Penicil_amidase; 1.

Hydrolase; Antibiotic resistance; Zymogen; Calcium-binding; Signal.

SIGNAL 1 24 POTERTIAL.

SIGNAL 25 802 PENICILLIN G ACYLASE ZYMOGEN.

CHAIN 25 234 PENICILLIN G ACYLASE ALPHA SUBJNIT.
                                                                                                                                                                                                                                                                                                                                                                                060136; 098463;
16-0CT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2004 (Rel. 43, Last annotation update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
(Penicillin G amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martin L.M., Prieto A.M., Cortes E., Garcia J.L.; "Cloning and sequencing of the pac gene encoding the penicillin G acylase of Bacillus megaterium ATCC 14945."; FEMS Microbiol. Lett. 125:287-292(1995).
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-!- COFACTOR: Binds 1 calcium ion per subunit (Potential).
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (By
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ne from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kang J.H., Kim S.J., Park Y.C., Hwang Y., Yoo O.J., Kim Nucleotide sequence of the penicillin G acylase gene fro Bacillus megaterium and characteristics of the enzyme."; Misainmurhag foiji 32:215-221 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                             1190 LeuGluGluGluArgSerValLeuAsnAsnGlnLeuLeu 1202
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-!- SUBCELLULAR LOCATION: Extracellular (Potential).
-!- SIMILARITY: Belongs to peptidase family $45.
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169 ThrTyrPheMetAspAsnHisGlnGluLeuLysAsnAlaGluIleLeuAlaLySLeuGlu
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PENICILLIN G ACYLASE BETA SUBUNIT.
SY SIMILARITY.
CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
                                                     T -> M (IN STRAIN CA4098).

D -> E (IN STRAIN CA4098).

I -> K (IN STRAIN CA4098).

T -> S (IN STRAIN CA4098).

A -> T (IN STRAIN CA4098).

A -> T (IN STRAIN CA4098).

C -> N (IN STRAIN CA4098).

C -> P (IN STRAIN CA4098).

I -> A (IN STRAIN CA4098).

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T -> K (IN STRAIN CA4098).

MXA -> XKS (IN STRAIN CA4098).

NXA -> XKS (IN STRAIN CA4098).
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62
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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35.44%
21.75%
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Query Match:
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Q8zcia yersinia pe
Q8zdwi bacteriopha
Q8qtz mycoplasma
Q81297 plasmodium
Q81hy4 plasmodium
Q9pic9 campylobact
Q9pi94 campylobact
Q9rg9 oryza sativ
G51329 borrelia bu
Q83rg7 streptomyce
Q81g7 streptomyce
Q81g5 plasmodium
G61768 caenorhabdi
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QRianl plasmodium
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          Q8flc7 escherichia
026108 helicobacte
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Q8ijz2 plasmodium
O43633 homo sapien
  shigella fl
escherichia
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Q8ilz2 plasmodium
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Q9fx81 arabidopsis
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Q97uf7 sulfolobus
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MBDinns=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
J. Bacteriol. 185:2330-2337(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601, 602;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MNS-2003 (TrEMBLrel. 24, Last annocation update)
Hypothetical protein (Positive regulator for sigma H (Sigma 32)
promoters, permitting growth at high temperature).
T0010 OR HTGA OR STM0010 OR STW0010.
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Q81EC2
Q9TPC2
Q9RH57
Q9Z188
Q84LB2
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Q9PI94
Q9ARQ9
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                            using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Database :

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463 ACGCTGTTTAAA---ATGGGGGGTTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAAT 519
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                                                                                                                                    160 SerieuAlaLysGlyValSerHisLeuLeuSerThrGlnLeuThrArgileLeuArgThr
                                                                                                                                                                                                  GCGGTCGCAAAAACCATTCTAGGGCGTGGTTTATCGCTTGCGGGCAATCAGGTGCTTACA
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STRAIN-301 / Serotype 2a;
MEDLINE=22772406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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C STRAIN=2457T / ATCC 700930 / Serctype 2a;
MEDLINE=25590274; PubMed=12704152;
A Med J., Goldberg MB., Burland V., Venkatesan M.M., Deng W.,
A Mau B., Pernain B., Paland V., Venkatesan M.M., Darling A.,
Fournier G., Maybew G.F., Plunkett G. III, Rose D.J., Darling A.,
A Mau B., Pernain N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
T (Complete genome sequence and comparative genomics of Shigella
T flexaris derotype 2a Strain 2457T.";
Infect: Immun. 71:275-2786(2003).
EMBL; AR015039; AAN416571;
REMBL; AR015039; AAN415571;
REMBL; AR015039; APPLES57.1;
REMBL; PRO05367; UPF0174; I.
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3 ValThrTyrLeuHisAspGluAspLeuAspPheLeuGlnHisCysSerGluGluGlnLeu 22
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                  SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Eatreille P., Courtrey L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
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NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Cyail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella
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Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
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ThrTrpLysLysMetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg 144
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|TyrLeuAsnAspSerAspLeuAspPheLeuGlnHisCysSerGluGluGlnLeuAlaAsn
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       Ö.
       Strond
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., St Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome of uropathogenic structure revealed by the complete genome of uropathogenic structure revealed by the complete genome selection wat! Aada Sci. U.S.A. 99:17020-17024 (2002).
InterPro; IPR005367; UPF0174.
InterPro; IPR005367; UPF0174.
Ffam, PF03667; UPP0174.
BHYDOCHELICAL DECEMBER 237 AA; 26727 MW; BRC190712375B31D CRC64;
                                                                                                                                                                                                                                                                                                    237
76
44
91
36
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Matches:
Conservative:
Mismatches:
Indels:
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165 ValSer----
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Best Local Similarity:
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1 AIGGCATACAAATAIGATAGAGACTIGGAATTTTTAAAGCAATIGGAAICTAGIGATTTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97394477; PubMed=9252185;
MEDLINE=97394477; PubMed=9252185;
Tomb Ju-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchun K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Gotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the gastric pathogen Helicobacter
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
STRAIN=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.
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HTGA OR Z0012 OR ECS0011.
Escherichia coli 0157:H7.
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                                                                                               01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-07NN-2003 (TrEMBLrel. 24, Last amotation update)
Hypothetical protein HP1590.
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01-MAR-2002 (TrEMBirel. 20, Last sequence update)
01-JUN-2003 (TrEMBirel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pylori.";
Nature 388:539-547(1997).
EMBL; AE000565; AAD08629.1;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
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Pred. No.:
Score:
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RESULT 4

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ID 2081

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ACGCCTGTAATGATCCAGCCAACAGACCTGTTAAAAAGCTCAGAGTTCTTGTAAGCACC 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 AspIleSerLeuSerAlaPheSerPheAsnArgPheGluThrSerSerLysMetAlaArg 122
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                                                                                                                                   SETRAIRE SERVE N.A.
SETRAIRE-015:117 / RIND 0509952;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo B., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Sasakawa C., Olasawara O., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. B:11-22(2001).
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|-----LeuSerPhelleSerSerGlySerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 TCTTCAGCGATTCTTCTGCGTATTTAGCGTAATCATCGCCATGC------CTT
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533 (2001).
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                     shock; Complete proteome.
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PIR; D90630; D90630
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                                                                                                                                                                                                                                                                              146 SerProAlaIleSerCysGlnLeuArgArgCysCysSerGlyCysProSerIleAspLeu 165
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                                                                                                                                                                                                                                                                                                                                           ------CITITGIAITCIAIG------GAGCIGGICAGIITTITCAIIGIGICIT
                                                                                                                                                                                                                                                                                                                                                                                                         166 AsmSerSerLeuArgIleSerMetLeuGluArgArgValLeuProPheSerLeuTrpVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 TTTTCGCCGTCTTTACCAAAACAAGCACCTCAAACAAATACAATAAATCACTAGATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluLysLysGluGluLysIleMetLysLysLeu---TyrSerGluHisProAspLeu
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VallysAspLeuMetAsnTyrGluLysGluTyrAlaGluLysArgAsnLeuLeuAsnAsn
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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Seeger K., Murphy L., Harris D., Berriman M.,
Sudail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ
EMBL, AL844507; CAD51332.1; -.
Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 AATTGC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                 SerSerArgAlaLysPheAlaAsnCysSer---SerLeuGlnCysTrpArgLysSerArg 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513
AsnSerSerLeuArgIleSerThrLeuGluArgArgValLeuProPheSerLeuTrpVal 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629 ACGCCCGTAAAGATCCAGCCAACAGGACCTGTTAAAAAGCTCAGAGTTCCTTGTAAGCACC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 ACAATGACAGCTAATTGATAAGATTTAAAA-----CCCCCCCATTTAAACAGGGGTTAAA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TCTTCATCC 372
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                                                          ACAAGCACCTCAAACAAATCCAATAAATCACTAGATTCCAATTGCTTTAAAAATTCCAAG
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|-----LeuSerPheIleSerSerGlySerSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCGCCGCGCTTAAAGCCTTGTCTGTTTAAATTGTCCGTGTTTTTTATGGATAATTCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 LysMetArgValSerTrpLeuGluSerLysCysAspThrProPheAlaAsnAsn----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 ATTTCTTCCAAACTTCTTTCTAAGATTTTAGAAAGCATGTTTTGTTCAATTAAAGTCGTT
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SERAIN=24577 / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

Rau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blatner F.R.;

"Complete genome sequence and comparative genomics of Shigella

Ileneri serotype 2a strain 2457I ";

Infect. Immun. 71:277-2786(2003).

EMBL; AB016978; AAP15558.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella flexneri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Positive regulator for sigma 32 heat shock promoters.
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Conservative:
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Best Local Similarity:
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Db 145 IleSerAspPheLeuLysGluAsnPheAsnIleGluLeuSerProGluValIleGluArg 164  Qy 331 AACATGCTITCTAAAATCTTAGAAAGAAATGGATGATGATGATGATGAAGAGTG 387  :::::     :::   :::   :::   :::     Db 165 HislleLysLeuAlaLysValLysAspLeuAspLysProPheLeuGlnAspLeuAsnGln 184  Qy 388 AAAGAAATGTGCGATGAATTATCCATAAAAAACACGGACAATTTA 432     :::   :::   :::      :::	433 AACGACATAAGCCCTGGCGG	Db 225 PheAspValLysGlnGluPheValPhePheLysAsnGluGlyLysProVal 241  Qy S02 GCTGTCATTGCGAATGCGGAGGGCGTGGCTTTTATGGCTTTGTGGGTGG	Qy 562 GGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTTAACAGGTCCTGTTGGCTGGATCATT 621	Oy 622 ACAGGCGTATGGACAGCGATTGATATTGCAGGGCCGGCTATAGGGTAACCATACCGGCA 681	Qy 682 TGCATT	Oy 700 TTA	QY         721 GCCAATGGAGATAAGAAGTCGTTGCAAATAGAATCCATT         759	DIMA PRELIMINARY; PRT; 276 AA. QBDIH4, QBDIH4, QBDIH4, QBDIHA; QL-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Tll614 protein.		SEQUENCE FROM N.A. STRAIN=BP-1, STRAIN=BP-1, MEDLINE=22255144; PubMed=12240834;	Nakamida 1., Kalisko i., Sato S., Ikeuni M., Ka Watamabe K., Iriguchi M., Kawashima K., Kimura Kiyokawa C., Kohara M., Matsumoto M., Matsuno P Shimpo S., Sugimoto M., Takeuchi C., Yamada M.,	"Complete ger Thermosynech DNA Res. 9:1: EMBL; AP0053:	SEQUENCE 276 AA; 31282 MW; D0577A9D97E0CA92 Cament Scores:	Pred. No.: 6.11 Length: 276 Score: 102.50 Matches: 50 Percent Similarity: 39.16% Conservative: 53
	RESULT 8 QBR9Z4 DB QBR9Z4 TD QBR9Z4 AC QBR9Z4; DT 01-UTN-2002 (TrEMBLrel. 21, Created) DT 01-UTN-2003 (TrEMBLrel. 24, Last sequence update) DT 01-UTN-2003 (TrEMBLrel. 24, Last amnotation update)	DE Hypothetical protein TTE1436.  NTTE1436.  S Thermoanaerobacter tengcongensis.  C Thermoanaerobacteriaceae; Clostridia; Thermoanaerobacteriales;  C Thermoanaerobacteriaceae; Thermoanaerobacteriales;  CX NCBL TAXID=119072;	RN [1] RP SEQUENCE FROM N.A. RC STRAIN-MB4 / JCM 11007; BY MENTINE-31003016. Behanda 1100330	Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., D Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X Tan H., Chen R., Wang J., Yu J., Yang H.;	XI "A complete sequence of T. tengcongensis genome.";  Genome Ress. 12:689-700 (2002).  DR EMBL; AR013102; AAM24658.1;  DR GO:0009424; C:flagellar hook (sensu Bacteria); IEA.	GO; GO:0003774; GO; GO:0009296; InterPro; IPR001 Pfam; PF02120; I	Hypoth	Alignment Scores:  Pred. No.:  103.50  Matches: 5.08  Matches: 63  Score: 2ercent Similarity: 35.14%  Conservative: 47  Best Local Similarity: 20.13%  Mismatches: 98  Query Match: 16  Gaps: 12  US-09-732-091-3 (1-759) x Q8R924 (1-403)	Oy 28 GAATITITAAAGCAATIGGAATCTAGTGATTTATTGGATTTGTTTGAGGGCTTGTTTT 87  [	Cy 88 GGTAAAGACGCGAAAAAAGCACAAAGAAAA	Qy 121TGACCAGCTCCATAGAATACAAAGGGAT 150 :::       :::    ::::::::::::::::::::	Qy 151 GGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATGGGAGC 210 Db 113 AlaSerAspPhedluLysValargGluLysLeuGluValAlalaLeuGln 128	Qy 211 AATAGTTTTGCGAGTTTCATJAAAGGCGAAGGAGTCTTATACAAAGACATTTTATGCGAT 270 Db 129GlyPhelleLysGluArgAsmPheThrPheLysGlulleAlaLysLys 144	Qy 271 GTGTGGGATAAATTAAAGGTCAATTACAACAAGAAAACTGAAACGACTTTAATTGAACAA 330

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|LeuMetArgValCysArgTyrLeuLysIleLysPheSerProSerTrpThrValProGlu 117
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212 AlaMetGlyValAlaArgLeuAlaValGlyArgSerIleLeuAlaPheValSerThrAla 231
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                                                                             24 LeuGluLeuAlaThrGluGluGluLeuGlnAspLeuThrGluIleLeuPhe-----
                                                                                                                        -----ArgArgLeuAsnProLeuAspTyrLeuThrThrProAspFrolleAlaVal
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                                                                                                                                                       148 CATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATGGG
                                                                                                                                                                            GlnAlaGlnAspArgGlnAlaTrpLeuAspAspileGluGluArgPheArgPheLeuAla
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Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
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| ProlleSerMetGluMetValArgLeuValLeuGluGlyGly----
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                                           Pubmedal 1032131;

Rad Dacks J.B., Marinets A., Ford Doolittle W., Cavalier-Smith T.,

Rad Logsdon J.M. Jr.;

Rad Jages of RNA Polymerase II Genes from Free-Living Protists:

Ry Logsdon J.M. Jr.;

Ry Jages of RNA Polymerase II Genes from Free-Living Protists:

Bylogeny, Long Branch Attraction, and the Bukaryotic Big Bang.";

Roll Biol. Evol. 19:830-840(2002).

ROL GO:0005634; Cluncleus; IEA.

GO: GO:0005634; Cluncleus; IEA.

GO: GO:0005634; Cluncleus; IEA.

GO: GO:0005634; Cluncleus; IEA.

GO: GO:0005636; Pirmancription from Pol II promoter; IEA.

GO: GO:0005636; Pirmancription from Pol II promoter; IEA.

GO: GO:000536; Pirmancription; IEA.

ROL GO:000536; Pirmancription; IEA.

GO: GO:000536; Pirmancription; IEA.

ROL GO:000536; Pirmancription; IEA.

GO: GO:000536; Pirmancription; IEA.

RICEPPO: IPRO07068; RNA POL Rpbl. 1.

InterPro: IPRO07068; RNA POL Rpbl. 4.

InterPro: IPRO07069; RNA POL Rpbl. 5.

InterPro: IPRO07078; RNA POL Rpbl. 5.

InterPro: IPRO07078; RNA POL Rpbl. 7.

Refam; PF04999; RNA POL Rpbl. 7.

Refam; PR04999; RNA POL IIREPEAT; 7.

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DB: Gaps: 6  US-09-732-091-3 (1-759) x QBIKGB (1-1455)  QY	OY 136GRATACAAAAGGCATGGCTAAATACGCTAAATACGCAGAAAGAA	QY         253 AAAGAGATTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC	Db 436GlnGluGluGluTyrLysSerLeuLeuAspGluLeuGluAsnAsn 452  Qy 424 GAC 426  Db 453 Glu 453	P87397  AC P87397  AC P87397;  DT O1-MAY-1997 (TrEMBLrel. 03, Created)  DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  DT 01-MAY-1997 (TrEMBLrel. 25, Last annotation update)  DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  DE Heat shock protein hsp90.  OS Oncorthynchus tschawytscha (Chinook salmon) (King salmon).  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  NN NCBI TaxID=74940;	RP SEQUENCE FROM N.A. RX MEDIATR=9926216; PubMed=10329464; RA MEDIATR=9926216; PubMed=10329464; RA Palminsano A.N., Winton J.R., Dickhoff W.W.; RT "Sequence features and phylogenetic analysis of the stress protein RT hispodalpha in chinook salmon (Oncorhynchus tshawytscha), a RT polkilothermic vertebrate."; RL Biochem. Biophys. Res. Commun. 258:784-791(1999). DR HSSP; POP9009; 18VQ. DR HSSP; POP9009; 18VQ. DR GO; GO:0001524; F:ATP binding; IEA. DR GO; GO:0001574; F:Anpeind Arpase.	InterPro; IRROGAGA; HSP90. Pfam; PF02518; HATPase c; 1. Pram; PR0183; HSP90; 1. PRINTS; PR00775; HEATSHOCK90. SWART; SM00387; HATPase c; 1. PROSITE; PS00288; HSP90; 1. SEQUENCE 726 AA; 83505 MM; Ignment Scores: 8.76
Qy         328 CAAAACATGCTTTCTAAAATCTTAGAAAGATTTGGAAGAAATGGAT	Cy 457 ACTTTAACGCTGTTTAAAATGGGGGGTTTTAAATCTTATCAATTAGCTGTCATTGTGCG 516	QY         577 ACAAGAACTCTGAGCTTTTTAACAGGTCCTGTTGGCTGGATCATT	SULT 11 IC39 GlyGluProAlaThrGlnM IK38 QBIKG8		RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., RA Chan MS., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S., RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., RA Martin D.M.A., Fairlamb A.H., Framholz M.J., Roos D.S., Ralph S.A., RA McFadden G.I., Cummings L.M., Subramanian G.M., Mingall C., RA Fraser C.M., Barrell B.J., Hoffman S.L., Newbold C., Davis R.W., RT "Genome sequence of the human malaria parasite Plasmodium RT "Annum": RL Nature 419:498-511(2002). RE EMBL, ARG14826; AA8737250.1.	ignment seq. No. seq. No. ore: ccent st. Loce

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                              Helicobacter
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STRAIN=ATCC 51449 / 331;

RA Suerbaum S., Josenhans C., Sterzenhach T., Drescher B., Brandt P.,

RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,

RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,

RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;

RT The complete genome sequence of the carcinogenic bacterium

RI The complete genome sequence of the carcinogenic bacterium

RI Helicobacter hepaticus.";

RI Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).

DR RMBL; AS017147; AAP77543.1;

KW Hypothetical protein; Complete protecome.

**RMBL; AS017147; AAP77543.1;

**RMBL; ANP77543.1;

**RMBL; ANP77543.1;

**RMBL; ANP77543.1;

**RMBL; ANP77543.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AspLeuGlnLysLeu-----AsnAlaPheAlaArgSerAspGluGlySerAlaSerGln
                                                                                                                                                                                                                                                    ||| ::::: ::: ::: SerAlaValIleAsnPheValLysGlyLeuGlnGlyPheAspSerGlnSerAlaThrIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| |||||||::
261 SerAlaAspGlnLeuSer-----AlaAsnGlnValSerLeuArgIleGluAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 AspGlnAlaArgThrLeuLeuSerValTrpLeu-------ValAlaAla
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                                              ----GICTIADACAAGAGATITITATGCGATGTGTGCGAT
                                                                                      164 ArgAspAlaIleValGlnAlaMetThrLeuPheGlnLysMetArgPheAspLeu----
                                                                                                                                   280 AAATTAAAGGTCAATTACAACAAGAAAACTGAAAACGACTTTAATTGAACAAAACATGCTT
                                                                                                                                                                             ---ArgGlyTyrThrTyrSerLeuLysAlaGluAsnArgAlaProAlaGluAlaSerMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
PRIO, 0048.
Plasmodium falciparum (isolate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                        436 AGACAAGCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGT
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EMBL; AE014829; AAN35246.1; -.
Hypothetical protein.
SEQUENCE 202 AA; 24259 MW; 48FD22A7F21165A6 CRC64;
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MEDLINE=22255705; PubMed=1236864;
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GluLeuleuGlyIleIleLeuLySSerLeuPheSerAlaAlaTrpValValSerThrLeu 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S., White C., Fraser C., Collmer A.; Rolengut J., Nelson W., Davidsen T., Complete sequence of Pseudomonas syringae."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, ARD16865; AAOS6120.1;
                                                                                                                                                                                                                                                                                                                                                                                     Gammaproteobacteria; Pseudomonadales;
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GC; GO:0004871; F:signal transducer activity;
GO; GO:0004871; P:signal transducer activity;
GO; GO:000165; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis_transd.
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PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
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Methyl-accepting chemotaxis protein.
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                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, Gammapro
Pseudomonadaceae, Pseudomonas.
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Best Local Similarity:
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Alignment Scores: Pred. No.: Score: Score: Score: Score Similarity: Guery Match: DB: US-09-732-091-3 (1-759)	AAATATGAT       ::: LysTyrGlu	TTTGAGGTG	GAAAAACTG 	AsnPheLeu'	GGGAGCAATI	TGCGATGTG: ::: AsnAsnLys]	CysLeuGly	TCTAAATC1      Lysaspilei	LeuSerAsp1	acggacaatttaaac                  
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7062, Ap 8, Appli 8, Appli 8, Appli 2, Appli 7, Appli 14, Appl 265, Appl 362, App

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Sequence 14, App]

Sequence Sequence

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GENERAL INCORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MACC J. Rubenfield et al.
APPLICANT: NUCLEA RESERVATION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29641
LENGTH: 273
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US-09-345-236B-98

US-09-346-301A-50

US-09-466-301A-50

US-09-099-933-4

US-09-099-933-4

US-09-099-933-1363

US-09-099-933-13363

US-09-0183-861-18

US-09-0183-861-18

US-09-183-861-18

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US-09-134-01C-326

US-09-133-14

US-09-263-33-17

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US-09-263-33-17

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US-09-025-769B-362

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US-09-01S-169-265
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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364.00
55.83$
35.42$
  Best Local Similarity:
  US-09-252-991A-29841
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US-09-252-991A-29841
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  TYPE: PRT
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DB:
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  Score
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-MODEL=frame+ n2p.mcdel -DEV=xlh
-Q=/Cqn2 1/USPTO spool/1809732091/runat 02072004 182407 19046/app query.fasta_1.903
-Q=/Cqn2 1/USPTO spool/1809732091/runat 02072004 182407 19046/app query.fasta_1.903
-DB=ISSUEd_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LODOCL=0
-LOOPEXT=0 -UNITS-Dits -START=1 -END=-1 -HATRIX=blosum62 -TRANS=tuman440.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LCOAL. OUTFWT=Patent - LOOPENCE - THR MINENG - MAXLEX=200000000
-USER-USO9732091_@CGN 1 1 18 @runat 02072004 182407 19046 -NCPU=6 -ICPU=3
-NO MARP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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12, Appl
16, Appl
5279, Ap
29, Appl
7696, Ap
749, App
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6437, Ap
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Sequence 29840, A
                                                                                5, 2004, 02:53:47; Search time 16.5 Seconds [without alignments] 4749.589 Million cell updates/sec
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                                                                                                                                                            1 atggcatacaaatatgatag.......cgttgcaaatagaatccatt 759
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                           protein search, using frame_plus_n2p model
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US-08-594-664-12

US-08-944-664-12

US-09-134-001C-5279

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US-09-134-01C-5279

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US-09-138-135-138-135-5845
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                                                                                                                                                                                                                                                            389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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Perfect score:
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Sequence 8852, Application US/09489039A

Sequence 8852, Application US/09489039A

Setent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 1099-01.27

PRIOR PLING DATE: 1999-01.29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8852

LENGTH: 258
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73 IleArgLeuLeulleAspVallleThrAspAsnGlyAsnGlyArglleSerLeuSerSer
                                                       1 ATGCCATACAAATATAGAGACTTG---GAATTTTTAAAGCAATTGGAATCTAGTGAT
                                                                              178 AGAATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAA---
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                     US-09-732-091-3 (1-759) x US-09-252-991A-29840 (1-321)
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; ORGANISM: Klebs:
US-09-489-039A-8852
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29840
LENGTH: 321
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     147
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142 ArgGluLeuGluGluIleLeuArgGluAlaGlyLeuAspLysThrLysMetThrAlaLeu 161
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                         .48 CATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATGGG
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GGTAAAGACGGCGAAAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAAAGG
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ORGANISM: Pseudomonas aeruginosa
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Query Match:
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684 SerLysLeuThrAlaValLeuAspIleIle-GlnLysLeuMetAspLysIleMetGl 703
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639 GluileSeriysLysAlaSerileMetLeuAsnArgThrValValAlaSerIysLeuThr
                                                                                                                                                                                                                                                                                           76 GTGCTTGTTTTGGTAAAAGCGGCGAAAAAGACACAATGAAAAACTGACCAGCTCCATA
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                                                                                                                                                                                                                                                                      16 GATAGAGACTIGGAATITITAAAGCAATIGGAATCIAGIGAITITAITGGATTIGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                ------AspLysLeuLysMetAlaThrLysIleLeuValThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 CAATACTATGGGAGCAATAGTTTTGCGAGTTTTCATTAAAGGCGAAGGAGTCTTATACAAA
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566 ValLeuPheValAlaAlaThrAlaLeuSerPheVallleGlyProAlaMet------
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Matches:
Conservative:
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Patent No. 5914238
GENERAL INFORMATION:
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                                                                 ORGANISM: Proteus mirabilis
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APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
         NOS: 8344
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Query Match:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TILLE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBE: 105/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                  ITGITTGAGGTGCTTGTTTTGGTAAAGACGGGAAAAAAGACACAATGAAAAAACTGACC 128
                                                                                                                                                                                                                                               AGCICC-----AIAGAAIACAAAAGGCAIGGCGAIGAIIACGCIAAAIACGCAGAA 177
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154 SerHisGluLeuAspSerLeuMetAlaHisLeuLeuArgHisArgLysLeuSerGluGly 173
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   Matches:
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Patent No. 6605709
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47.58%
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           Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-543-681A-6437
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CITY: BO
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105 luGluAspGluGluSerAspAlaValValSerGlnValLeuAspGluLeuGlyLeuS 125
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                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FLING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,98
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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Mismatches:
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TITLE OF INVENTION: MATERIALS AND METHODS TITLE OF INVENTION: BREAST CANCER TITLE OF INVENTION: BREAST CANCER CORRESPONDENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSEB: Testa, Hurwitz & Thibeauit STRET: 125 High St. CITY: Boston STATE: MA
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
Query Match:
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                                APPLICANT: GBAR, NOBERT
APPLICANT: GRAR, NOBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/944,604
FILLING DATE:
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
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NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,98
REFERENCE/DCCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 12:
SROUBNUCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 GGAGC---AATAGTTTTGCGAGTTTCATTAAAGGC--
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Gaps:
                                                                                                                                         ; Sequence 12, Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
APPLICANT: KERSEE, SUSAN
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
RIOR FILING DATE: 1997-11-4
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5279
                                                                                                                                                                                                                                               GIGCITGITTTTGGTAAA---GACGGCGAAAAAGACACAATGAAAAACTGACCAGCTCC 132
                                                                                                                                                                                                                                                                                                                                                                                            110 MetGlyThrMetAsnArgGlnLeuLysLeuProGlnIleGlnLyslleMetMetGluPhe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIGAAAGAAATGIGCGAI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 GluLeuGlyLeuSerLeuThrAspGluLeuSerAsnLeuProSerThrGlyGlySerLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 ACGCIGITIAAAAIGGGGGGTITIAAAICTIAICAAIIAGCIGICACAITGCGAAIGCG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 Serval---AlaAlaGlyGlyLysLysAlaGluAlaAlaAlaAserAlaLeuAlaAspAla 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AACAAGAAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAAATCTTAGAAAGA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATTATCCATAAAAAACACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCGACTTTA 462
                                                                                                                                                                                                                                                                                             70 ArgArgTyrValArgLysPheValLeuMetArgAlaAsnIleGlnAlaValSerLeuLys 89
                                                                         50 MetalalysGlnGlyGlnMetAspAlaValArglleMetAlaLysAspLeuValArgThr
                                 193 TTGCAATACTATGGGAGC---AATAGTTTTGCGAGTTTCATTAAAGGC
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Mismatches:
Indels:
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Matches;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 5279, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
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23.85$
7.34$
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-134-001C-5279
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ORGANISM:
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                                                                                                                                                                                             -GTGAAAGAAATGTGCGATGAATTATCCATAA 415
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                                                  251 ACAAAGAGATITITAIGCGAIGIGCGATAAAITAAAGGICAATTACAACAAGAAACIG 310
                                                                                                                                                              416 AAAACACGGACAATTTAAACAGACAAGCCTTAAGCGGGGGACTTTAACGCTGTTTAAAA 475
ysSerAsnAsnSerMetAlaGlnAlaMetLysGlyValThrLysAlaMetGlyThrMetA 65
                                                                                    sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sittii: sittiii: sittiii: sittiii: sittiii: sittiii: sittiii: sitt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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339
48
112
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches:
Conservative:
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Indels:
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STREET: 125 High St.
CITY: Boston
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Patent No. 6218131
GENERAL INFORMATION:
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NAME: MEYERS, THOWAS C
REGISTATION NUMBER: 36,989
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
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47.80%
21.43%
7.34%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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FILING DATE:
CLASSIFICATION: 435
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US-08-944-604-16
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Sequence 7696, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA;
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION UNMERR: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1999-04-05
PRIOR APPLICATION UNMERR: US 60/128,706
PRIOR APPLICATION UNMERR: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                             |||::: ||||||:::
1086 ArgCysGluAlaLeuLysIleGlnAlaAspGlyPheLysAspGlnLeuArgSerThrAsn 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1123 LysCysLeuGluGluAspLeuAlaLysSerGlnAsnLeuValSerGluPheLysGlnLys 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||::: :::|||
|1143 CysAspGlnGlnAsnIleIleIleGlnAsnThrLysLy9GluValArgAsnLeuAsnAla 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AATTACAACAAAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAAATC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 AAATACGCAGAAAGAATCGCTGAAGAGTTG-----CAATACTATGGGAGCAATAGTTTT 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- AAAAACACGGACAATTTAAACAGA 438
                                                                                                                                                                                                                                      GCATACAAATATGATAGAGACTIGGAATTTTTAAAG-----CAATTGGAATCTAGTGAT 57
                                                                                                                                                                                                                                                                                                                                                                                106 AGACACANTGAAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCT
                                                                                                                                                                                                                                                                                                            TIAITGGATITIGITT-----GAGGIGCTIGITITITIGIAAAGACGGCGAAAAA
                                                                         2125
46
35
62
38
   ; OTHER INFORMATION: Incyte ID No. 6673545 3774181CD1
US-09-919-172-29
                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                  US-09-732-091-3 (1-759) x US-09-919-172-29 (1-2125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 GIGIGGGATAAATTAAAGGIC----
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                                                                                        95.00
44.75%
25.41%
7.04%
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US-09-543-681A-7696
                                                                                                       Percent Similarity:
Best Local Similarity:
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1163 Glu 1163
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US-09-543-681A-7696
                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROT : 1286
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                                                                                                                                                                             28 ThrSerArgGluAlaLeuIleLysAspValValMetIleAlaAlaArgIleLeuLeuGlu 47
TACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTGGAT
                                                                                            48 SerGlyAlaGluGlyThrArgValGluAspThrMetAlaArglleAlaThrLysLeuGly
                                                                                                                                                                                                                                                                                     199 TACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAG
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Patent No. 6673545
PATENT NORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
APPLICANT: PROFIT CANGER MARKERS
FILE OF INVENTION: PROSTATE CANGER MARKERS
FILE REPERENCE: PA-0036 US
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: BERL PROGRAM
SEQ ID NO 29
LENGTH: 2125
                      88 AlaTyrProArgLeu-----
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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US-09-919-172-29
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US-09-328-352-5845
US-09-328-352-5845
US-09-328-352-352-352-352
FATENT NO. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 GATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAACACGGACAATTTA 432
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||AspLeuSerValLysPheSerSerPheValAspAlaThrGlnMetAlaGluAlaAla 196
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70 ValAspAspGluzleAlaGluValGlySerLysGluGluGluGluGserGlnGluPhe
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56
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                                                                                                            Conservative:
Mismatches:
Indels:
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Matches:
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                     ; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-749
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89.50
41.18%
21.96%
6.63%
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Best Local Similarity:
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Patent No. 6559294

GENERAL INRORMIGN:
APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 749
LENGTH: 281
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|LeuTyrGlnGlnAlaSerValAspbeuGlyGluLysGluLeuValAsnLeuGlnArgAsn 842
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443
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PheAlaTyrAspArgGlybysGlu---IleGluGlnMetGln-
                                           Conservative:
Mismatches:
Indels:
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                  Length:
Matches:
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6.78%
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                                         Percent Similarity:
Best Local Similarity:
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US-09-198-452A-749
Alignment Scores:
Pred. No.:
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and Methods for Control of Invertebrates
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113 ProGluAsnLeuAsnAspIlelleThrAspGlnLeuArgAspPheMetAlaGlnGluLeu 262
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ValAspFyrAsnGlnValValLeuHisIleLeuAspAsnTyrAspGlnArgLeuGluGlu 322
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Matches:
Conservative:
Mismatches:
Indels:
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   TITLE OF INVENTION: Compositions, and Meth
FILE REFERENCE: 21042.0004
CURRENT APPLICATION NUMBER: 08/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: ZastSEQ for Windows Version 3.0
                                                                                                                                TYPE: PRT
ORGANISM: mosquito baculovirus
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23.53%
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Best Local Similarity:
Query Match:
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US-09-345-236B-98
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|AsplysSerLeuGluGluLeuGluLysGluGluArglysAspLeuLysAsnArgPheAsp 385
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GluTyrProValValSerGlyValPhe-----LysLeuLeuCysAspThrAlaGlnSer 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 AGITICATIAAAGGCGAAGGAGICTIAIACAAAGAGAITITAIGCGAI----
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REPRENEUR: GT039-032A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 543
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Patent No. 6521454
GENERAL INFORMATION:
APPLICANT: Bencel, James J.
APPLICANT: Moser, Bettina
APPLICANT: Moser, Bettina
APPLICANT: White, Susan E.
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
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40
31
52
52
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                            ) ORGANISM: Acinetobacter baumannii
US-09-328-352-5845
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89.50
37.37%
21.05%
6.63%
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Best Local Similarity:
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US-09-345-236B-98
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                                                                                                               TYPE: PRT
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Sequence 50, Application US/09446301A

Sequence 50, Application US/09446301A

Patent No. 6506093

GENERAL INFORMATION:
APPLICANT: BL.SOLH, NEVINE
APPLICANT: ALLIGNET, JEANINE
TITLE OF INVENTION: POLYNCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: COMPOUNDS
FILE REPRENCE: 03715-0059
CURRENT APPLICATION NUMBER: US/09/446,301A
CURRENT PILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51

CONTRANT PILING NAME: 1999-12-20
SOFTWARE: PATENTIN VET. 2.1
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US-09-446-301A-50
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LENGTH: 560
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                                    Sequence 121, Application US/09345236B

Petent No. 6521454

GENERAL INFORMATION:
APPLICANT: Becnel, James J.
APPLICANT: Mescr. Jettina
APPLICANT: Mescr. Jettina
APPLICANT: Mite, Susan E.
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
APPLICANT: Occhuru, Jandeen, Albert H.
APPLICANT: Occhuru, Compositions, and Methods for Control of Invertebrates
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
CURRENT FILE REPREBENCE: 21042.0004
CURRENT FILENG DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 121
EDECTH: 546
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ValPheGluValValGlyGlyGroGluGlyAspTyrAlaAlaGlyGluGluAspGlu 172
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|---ThrProProThrSerAlaGlnProAspMet 232
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283 AlaLeuAlaileThrValAlaAspArgValSerArgSerPheMetTyrGluGlyArgile 302
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Mismatches:
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; ORGANISM: mosquito baculovirus
US-09-345-236B-121
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    RESULT 14
US-09-345-236B-121
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Search completed: July 5, 2004, 03:07:23 Job time : 21.5 secs

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Sequence 44, Appl Sequence 9162, Ap Sequence 9163, Ap Sequence 9164, Ap Sequence 7699, Ap Sequence 7698, Ap
                                                                                                                          Sequence 20, Appl Sequence 17, Appl Sequence 19, Appl Sequence 18, Appl Sequence 16, Appl Sequence 16, Appl Sequence 43832, A Sequence 191043,
                                                                                                                                                                                                                                     Sequence 76490, A
Sequence 42, Appl
Sequence 7400, Ap
Sequence 14395, A
Sequence 54543, A
Sequence 29, Appl
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Sequence 220, App
Sequence 230, App
Sequence 16094,
Sequence 52737, A
Sequence 47217, A
Sequence 5229, Ap
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Sequence 1075, Ap
Sequence 222059,
Sequence 107, App
Sequence 43207, App
Sequence 43207, App
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58561, A
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749, App
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Sequence 12141, A
Sequence 197045,
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APPLICANT: Tian Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
FILE REPERENCE: 7969-088
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
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2 US-10-335-977-9164

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2 US-09-732-091-19

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4 US-10-282-122A-54543

2 US-10-282-122A-54543

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; Patent No. US20020107368A1
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1279.00
 ORGANISM: Helicobacter sp
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-Q=/GG12 1/UGFTO spool/USG9732091/runat 02072004 182407 19065/app_query.fasta 1.903
-DB=Published Applications AA -OFMI-fastan -SUPFIX.abp.rapb -MINMATCH=0.1
-LOOPOLL=0 -LCOPEXT=0 -UMITS=bits -STRAKT=1 -END=-1 -MATRIX=biosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR MX*=100
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-MAXLENE=2000000000 -USER=US0973201 @CGN 1 1 135 @runat 0207204 182407 19065
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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                                                                                             July 5, 2004, 03:03:18; Search time 67.5 Seconds (without alignments) 7000.427 Million cell updates/sec
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1: /cgn2_6/ptodata/2/Pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/Pubpaa/PCT_MBW_PUB.pep:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                   - protein search, using frame_plus_n2p model
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Post-processing: Minimum Match 0%
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Scoring table:

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                                               US-09-732-091-3 (1-759) x US-09-732-091-4 (1-253)
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RESULT 3 US-10-335-977-9162 Sequence 9162 Application US/10335977 Publication No. US20040052799AL

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US-10-335-271-3463

US-10-335-271-3463

SEQUENCE 9163, Application US/10335977

SEQUENCE 9163, Application US/20335977

SEQUENCE 1 SECRETARY OF 1 SEQUENCES

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AlaAsnGluAspLysLysSerLeuGlnIleGluSerVal 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCAATGGAGATAAGAAGTCGTTGCAAATAGAATCCATT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9163:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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STATE: Massachusetts
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                                                                                                                    361
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         APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICCBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature

COCATION: (B) LOCATION 1...253

SECUROE DESCRIPTION: SEQ ID NO: 9162:
US-10-335-977-9162
                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
                                                                                                         & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                             3: (617)227-7400
(617)742-4214
                                                                                                      ADDRESSEE: LAHIVE & COC
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9162: SEQUENCE CHARACTERISTICS:
                                                                         SEQUENCES: 10031
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                                                                                      CORRESPONDENCE ADDRESS
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99.60%
99.21%
94.14%
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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           RESULT 5
US_10_335_277-9164
i Sequence 9164 | Application US/10335977
i Publication No. US20040052799A1
i GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNATICS AND THERAPEUTICS
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy B.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 9164:
SEQUENCE CHARCTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...256
SEQUENCE DESCRIPTION: SEQ ID NO: 9164:
                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
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1270.00
99.60%
99.21%
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                      2 ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA
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                                                                                                                                                                                                              Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                           Mismatches:
Indels:
Gaps:
                                                                                                          NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...253
SEQUENCE DESCRIPTION: SEQ ID NO: 9163;
                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                                                             6.11e-122
1270.00
99.60%
99.21%
94.14%
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                          US-10-335-977-9163
                                                                                                                                                                                          Alignment Scores:
Pred. No.:
                                                                                             FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                82 GITITIGGIAAAGACGGCGAAAAAAGACACAATGAAAAACTGACCAGCTCCATAGAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||::: :::|||||||
31 ValTyrAspGluAspGlyThrLeuArgMetAsnGluGluLeuThrScrLeuThrGluTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYrGlyGlyAsnSerPheAlaAsnPhePheArgAspGluGlyValLeuTyrLysGluIle
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141
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                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Xismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                        x US-10-335-977-7699 (1-248)
                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...248
SEQUENCE DESCRIPTION: SEQ ID NO: 765
                                                                                                                                             ORGANISM: Helicobacter pylori
            (617)227-7400
                                                                LENGTH: 248 amino acids
TYPE: amino acid
                      TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7699:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        1.9e-65
722.00
75.64%
60.26%
53.52%
                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                     US-09-732-091-3 (1-759)
                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                               US-10-335-977-7699
                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                           FEATURE
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                  ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
                                                    GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC
                                                                                                         aagaaaactgaaacgactttaattgaacaaaacatgctttctaaaatcttagaaagt
                                                                                                                          TTGGAAGAAATGGATGAAGAAGTGAAGAATTGTGCGATGAATTATCCATAAAAAC
                                                                                                                                                                                 ACGGACAATTTAAACAGGAAAGCCTTAAGCGCGGGGGACTTTAACGCTGTTTAAAATGGGG
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                                                                                                                                                                                                                                                                                                                                               TATAGGGTAACCATACCGGCATGCATTGTGGTTGCCACTTTACGCCTAAAAACACAGCAA
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10s-10-31s-977-7699
1 Sequence 7699, Application US/10335977
1 Publication No. US20040652799A1
2 GENERAL INFORMATION:
1 APPLICANT: DOUGLAS SMITH et al
2 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
2 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
3 PLACED AND THERAPEUTICS
5 PLACED AND THERAPEUTICS
6 PLACED AND THERAPEUTICS
7 PLACED AND THERAPEUTICS
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
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ADDRESSES: LASIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT
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MEDIUM TYPE: CD/ROM ISO9660
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ZIP: 02109-1875
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PAPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Encoding No. US20030158396Alel Helicobacter Polypeptides in t
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US 08/902,615
FRICK APPLICATION NUMBER: US 08/902,615
FRICK APPLICATION NUMBER: US 08/902,615
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                  GAACAAAACATGCTTTCTAAAATCTTAGAAAGAAGTTTGGAAGAAATGGATGATGAAGAA 384
                                             61 GlyGlyAsnSerPheAlaAsnPhePheArgAspGluGlyValLeuTyrLysGluIleLeu
                                                                                             TGCGATGTGCGATAAATTAAAGGTCAATTACAAGAAAAACTGAAACGGACTTTAATT
                                                                                                                                                                                          205 GGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAGATTTTA
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                                                                                                                                                                                                                                                                                                                  436 AGACAAGCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGTTTTTAAATCTTAT
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Helicobacter pylori
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Best Local Similarity:
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                                                              Sequence 7698, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
ThrValProAlaCysValLeuValAlaThrLeuArgLysLys 244
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dcc-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...237
SEQUENCE DESCRIPTION: SEQ ID NO: 7698:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
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TELEPHONE: (617)227-7400
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                        STATE: Massachusetts
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                        ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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                                    RESULT 7
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                                                                                                             Sequence 17, Application US/09732091
Patent No. US200201073681
GENERAL INFORMATION
APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-732-091-19

Sequence 19, Application US/09732091

Patent No. US20020107368A1

Patent No. US20020107368A1

APPLICANT: Tian, Jing-Hui

APPLICANT: Walker, Richard I.

APPLICANT: Jackson, W. James

TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses

TITLE OF INVENTION: thereof

TITLE OF INVENTION: thereof

CURRENT APPLICATION NUMBER: US/09/732,091

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 TTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAGATTTTATGCGAT
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Matches:
Conservative:
Mismatches:
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Matches:
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        41 GlyAspLysLysSerLeuGlnIleGlu
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; ORGANISM: Helicobacter sp.
US-09-732-091-19
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ORGANISM: Helicobacter
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Best Local Similarity:
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LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 LysAspSerLeuGluLysMetSerArgArgGlulleLysGluLeuCysAsnGluLeuGluLeuGluLysAsnGluLeuGluLeuGluLysAsnGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeuGluTeu
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                                                                                                                                          42 ArgAspGluG1yValLeuTyrLysGlu11eLeuCysAspAlaCysAspHisLeuIysVal 61
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                                232 AAAGGCGAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTC
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Farent No. US20020107368A1

GENERAL INFORMATION

APPLICANT: Tian, Jing-Hui

APPLICANT: Walker, Richard I.

APPLICANT: Walker, Richard I.

APPLICANT: Helicobacter proteins, gene sequences and uses

ITILE OF INVENTION: Thereof

FILE REFERENCE: 7969-088

CURRENT PILING DATE: 2000-12-07

NUMBER OF SEQ ID KOS: 44

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO: 20
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ORGANISM: Helicobacter sp.
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GENERAL INFORMATION:
APPELICANT: Wang, Liangsu
APPELICANT: Mang, Liangsu
APPELICANT: Mang, Liangsu
APPELICANT: Mand, Carlos
APPELICANT: Mando, Carlos
APPELICANT: Haselbeck, Robert
APPELICANT: Haselbeck, Robert
APPELICANT: Zyskind, Judith
APPELICANT: Zyskind, Judith
APPELICANT: Trankick, John
APPELICANT: Trankick, John
APPELICANT: Trankick, John
APPELICANT: Forzyth, R.
APPELICANT: Porzyth, R.
APPELICANT: Porzyth, R.
APPELICANT: WANGER: US/10/282,122A
APPELICANT: ROTOSYTH, R.
APPELICANT: ROTOSYTH, R.
APPELICANT: NAWBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/200,384
PRIOR APPLICATION NUMBER: 60/200,384
PRIOR PELING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/200,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,331
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257,331
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257,331
PRIOR PILING DATE: 2000-10-23
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
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SEQ ID NO 43832
LENGTH: 1009
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21 TyrGlnLeuAlaVallleValAlaAsnAlaValAlatysThrIleLeuGlyArgGlyLeu 40
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Sequence 16, Application US/09732091

Sequence 16, Application US/09732091

GENERAL INFORMATION:

APPLICANT: Tian, Jing-Hui

APPLICANT: Tian, Jing-Hui

APPLICANT: Walker, Richard I.

APPLICANT: Walker, Richard I.

TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses

TITLE OF INVENTION: Helicobacter proteins, gene sequences

TITLE OF INVENTION: 1969-088

CURRENT PALING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 16

LENGTH: 30
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// Sequence 18, Application US/09732091
// Patent No. US2002210358A1
// GENERAL INFORMATION:
// APPLICANT: Tian, Jing-Hui
// APPLICANT: Walker, Richard I.
// APPLICANT: Walker, Richard I.
// APPLICANT: Walker, Richard I.
// APPLICANT: Walker, Richard I.
// APPLICANT: Walker, Richard I.
// APPLICANT: Walker, Richard I.
// TITLE OF INVENTION: thereof
// TITLE OF INVENTION: thereof
// TITLE OF INVENTION: thereof
// TITLE OF INVENTION: WABER: US/09/732,091
// CURRENT FILING DATE: 2000-12-07
// NUMBER OF SEQ ID NOS: 44
// SOFTWARE: PatentIn Ver. 2.1
// LENGTH: 35
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ORGANISM: Helicobacter sp.
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; CRGANISM: Helicobacter sp.
US-09-732-091-16
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Best Local Similarity:
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Boukharov, Andrey Barbazuk, Brad

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------AGACAAGCC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...----IleArgArgGluAlaValSerHisGlyLeuGlu 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------CAAAACAIGCIITCIAAAAICIIAGAA 354
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|TyrAsnAsnAsnLeuGluLeuAsnGluGlnSerIleGluMetGluMetSerArgLeuAsn
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897 IleAspValPheAspLeuHisSerAsnLys-----SerArgHisIleSerSerLeuSer
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US-09-732-091-3 (1-759) x US-10-282-122A-43832 (1-1009)
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Sequence 191043, Application US/10437963
FUBLICATION NO. US20401123343A1
SEBERRAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAACACGGACAATTTAAAC-----
                                                         TATGATAGAGACTTGGAATTT-
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APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated Witl
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 191043
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617 -----GluSerThrSerGlnGluLeuValAspGluArgLysThrValThrThrLeuAsn 634
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26
62
27
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Matches:
Conservative:
Mismatches:
Indels:
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97.50
44.38%
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7.23%
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ORGANISM: Oryza sativa
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Best Local Similarity:
                                                                                                                                                                                                                                                                                           ; UIHEK INFORMATION ; US-10-437-963-191043
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                                                                                                                                                                                                LENGTH: 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
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